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June 18, 2003, 12:40:57 ; Search time 38 Seconds (without alignments) 1763.817 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•			Description	Modified Interfero	Human intracellula	Chimeric protein I	Human protein SEQ	Human IRF3 protein	Modified Interfero	Human ovarian anti	Murine lymphocyte	Human lymphocyte s	Human multiple mye
CHINALIES			DI CI	AAY15103	AAE09329	AAY15104	AAM78986	AAY87783	AAY15102	ABP42913	AAR99426	AAR99427	AAW38426
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	dip.	Query	Match	100.0	98.7	57.4	16.8	16.6	16.5	16.3	13.8	13.2	13.1
			Score	2731	2695	1567.5	458	454	450	446	376	361.5	357
		Result	No.		7	e	4	S	9	7	œ	60	10

Human IFN regulato Human IFN regulato	procein a	secreted	Human ovarian anti	Ψ	IRF-1 active prote	Human homologue of	Protein coded for	Human interferon r	Human interferon r	IRF-1 active prote	Murine interferon	Interferon-beta re	Human polypeptide	Human ORFX ORF1813	Human PKIN-24 prot	Rat synapsin 1B (Y	Human polypeptide	Human polypeptide	Collagen-like poly				Human protein sequ			gen-like		Human IRF-2 protei	Human endometrial	pr	gIV from BHV-1 str	
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ALIGNMENTS

Interferon regulatory factor, IRP-7, transactivation domain; serine; threonine; carboxy terminus; aspartic acid; mutant; phosphorylation; post-translational modification; sendai virus; cancer treatment; herpes; activator; promoter; ISRE regulatory element; stimulation; influenza; DNA binding; transcriptional activity; viral infection; HIV infection; activate; homology; cytokine gene; target cell. Modified Interferon Regulatory Factor-7 protein (IRF-7). AAY15103 standard; Protein; 503 AA (first entry) 25-JAN-2000 RESULT 1 **AAY15103** 

Homo sapiens. Synthetic

'note= "Wild type Ser replaced with Asp" /note= "Wild type Ser replaced with Asp" Location/Qualifiers Misc-difference Misc-difference WO9951737-A1 14-OCT-1999

99WO-CA00314. 07-APR-1999;

98CA-2234588. 07-APR-1998;

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sapiens.
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                                                                                                                                               The present protein sequence is the interferon regulatory factor-7 (FRF-7). 2D protein, that is modified in the transactivation domain. The serine and threonine residues in the carboxy terminus are modified post-translationally, by phosphorylation, following sendai virus infection. The modified IRF-7, substituted with aspartic acid, functions as a activator of promoters containing ISRs regulatory elements and stimulation of DNA binding and transcriptional activity. IRF-7 protein the treatment of viral infections like, influenca, herpes or HIV infection. They may also be used to activate a cytokine gene, in cancer treatment or to modify a target cell of an organism.
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                                                                                                               Human; intracellular regulator; cell division; proliferation; therapy; cancer; infection; wound; developmental abnormality; metabolic problem; cytostatic; antibacterial; vulnerary; transcription factor; KWC02; interferon response factor; IRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New genes encoding intracellular regulatory molecules, useful for regulating cell division and proliferation (e.g. tumor cells), particularly for treating cancer, infections, wounds, or developmental or metabolic abnormalities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a human intracellular regulatory molecule, KWC02. The KWC02, an interferon response factor (IRF) homologue, is a transcription factor. The polynuclectides encoding intracellular regulatory molecules are useful for regulating cell division and proliferation of various cell types, including tumour cells. Specifically, they are also useful for treating cancer, infections, wounds, developmental abnormalities or metabolic problems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MALAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAWAVARGRWPPSSRGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McClanahan TK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.7%; Score 2695; DB 22;
99.0%; Pred. No. 8.4e-195;
iive 0; Mismatches 5;
                                                         Human intracellular regulatory molecule, KWC02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lees EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Column 33-38; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shanahan F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0999774.
(first entry)
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Best Local Similarity 99.0
Matches 498; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seghezzi W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-535086/59.
N-PSDB; AAD16105.
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                                                                                                                                                                                      Interferon regulatory factor; IRF; chimeric protein; serine; threonine; carboxy terminus; amino terminal domain; aspartic acid; phosphorylation; post-translational modification; sendai virus; cancer treatment; herpes; PRDI/PRDII; promoter; ISRE regulatory elamont; stimulation; activate; activator; DNA binding; transcriptional activity; viral infection; proteasome_mediated degradation; influenza; HIV infection; cytokine gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the chimeric protein comprising, residues 1-246 from the modified amino-terminal domain of interferon regulatory factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulatory
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QRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSSLSL
                                                                                                                                                                                                                                                                                      /note= "Corresponds to modified amino-terminal domain
of IRP-7 protein"
247..542
                          QRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDL
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                                                                                                                                                                                                                                                                                                                                carboxy-terminus
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                                                                                                                                                                                                                                                                                                                               modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified highly active forms
                                                                                                                                                                       Chimeric protein IRF-7(1-246)/IRF-3(132-427).
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                                                           CLSSANSLYDDIECFLMELEQPA 503
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IRF-3 protein"
                                                                          CLSSANSLYDDIECFLMELEOPA 503
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                                                                                                                                                                                                                                                                                                                                                        note= "Wild type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor proteins used for the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98CA-2234588
                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-620201/53
                                                                                                                      AAY15104 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carboxy-terminus
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                                                                                                                                                                                                                                             target cell
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                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                      AAY15104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 TPFPNLGPSENPLKRLLVPGEEWEFEVTAFYRGRQVFQQTISCPEGLRLVG-SEVGDRTL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GODLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDLCLSSANSL---YDD 491
(5D) protein. The serine and threonine residues are post-translationally modified by phosphorylation, following sendia virus infection. The modified by phosphorylation, following sendia virus infection. The modified IRP, substituted with aspartic acid, functions as a strong activator of promoters containing ISRE and PRDI/PRDII regulatory elements, stimulation of DNA binding and transcriptional activity and proceasome mediated degradation. The modified IRF sequences are used for the treatment of viral infections like, influenza, herpes or HIV infection. They may also be used to activate a cytokine gene, in cancer treatment or to modify a target cell of an organism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PSACTAVQEPSPG---ALDVTIMYKGRTVLQKVVGHPSCTFLYGPPDPAVRAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETTPSPTSDTQEDILDELLGNMVLAPLPDPGPPSL----AVAPEPCPQ--PLRSPSLDNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 DPQQVAFPSPA-ELPDQKQLRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWBVG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MALAPERAAPRVLFGEWLLGEISSGCYEGLÓWLDEARTCFRVPWKHFARKDLSEADARIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 PGWPVTLPDPGMSLTDRGVMSYVRHVLSCLGGGLALWRAGQWLWAQRLGHCHTYWAVSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MALAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67;
                                                                                                                                                                                                                                                                                                                                                                                                                              57.4%; Score 1567.5; DB 20; Lengt
59.7%; Pred. No. 7.7e-110;
.ive 38; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM78986 standard; Protein; 427 AA
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                                                                                                                                                                                                                                                                                                                                                                       542 AA;
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523 YKAYLODL
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Matches 327;
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224 EGLRLVG-SEVGDRTLPGWPVTLPDPGMSLTDRGVMSYVRHVLSCLGGGLALMRAGQMLM 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 WPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSRELC 129
                                                                                                                                          419 ARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLBPWLCRVHLEGTQREGVSSLDSSDL 478
                                                                                                                                                                             334 EGSGR-SPRYALWFCVGESWPODOPWTKRLVMVKVVPTCLRALVEMARVGGASSLENT-V 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel polynucleotide (I) encoding human ADA2. The products of the invention have cytostatic activity and can be used for gene therapy. (I) is useful for treating cancer; as primers and probes for isolating full length cDNA and genes having similar biological activity. This sequence represents the human IRF3 protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polynucleotide encoding human AD2 is useful for treating cancer and isolating cDNAs and genes having similar biological activity
                                                           -----GPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFR
                                                                                                283 AQRLGHCHTYWAVSEELLPNSGHGPDGE------VPKDKEGGVFDLGPFIVDLITFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ADA2; cytostatic; gene therapy; treatment; cancer; IRF3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Column 59-62; 54pp; English.
                                                                                                                                                                                                                                              || :|::: | ::| :| DLHISNSHPLSLTSDQYKAYLQDL 415
                                                                                                                                                                                                                        DLCLSSANSL --- YDDIECFLMEL 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                              AAY87783 standard; Protein; 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                             ARRMGKCKVYWEVG-
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ses 141; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                          24-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                     AAY87783;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSRELC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 WREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----TQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEP-SPGALDVTIMYKGRTVLQKVVGHP 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCTFLYGPPDPAVRATDPQQVAFPSPA-ELPDQKQLRYTEELLRHVAPGLHLELRGPQLW 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||:|-pwlvsQlDlGQlEGvawvnKsrtrfrIPwK+GlRQDAQQEDFGIFQAwaEatGa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLRSPSLDNPTP-----FPNLGPSENPLKRLLVPGEEWEFEVTAFYRGRQVFQQTISCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 YVP----GRDKPDLPT----WKRNFRSALNRKEGLRLAEDRSKDPHDPHKIYEFV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVARGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                              C, Cao Y,
Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 458; DB 22; Length 427; Pred. No. 2.2e-26; 64; Mismatches 191; Indels 108;
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                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT, Asundi V, Zhou P,
Wang J, Zhang J, Ren F, Chen
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -NSGVG----DFSQPDTSPDTNGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 3986; 6221pp; English
                                                                                                                                                          2000US-0496914.
2000US-0560875.
2000US-0598075.
                                                                                                                                                                                                                    2000US-0620325.
2000US-0654936.
2000US-0663561.
2000US-0693325.
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                                                                                                                     2001WO-US04098
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N-PSDB; AAK52119.
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Best Local Similarity
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Wang D,
Yang Y, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       427 AA;
                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                         WO200157190-A2
                                                                                                                                                                               27-APR-2000; 20-JUN-2000; 219-JUL-2000; 21-SEP-2000; 20-OCT-2000; 30-NOV-2000; 2
    Homo sapiens.
                                                                                                                       05-FEB-2001;
                                                                                09-AUG-2001
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309
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                                                                                                                                                                                 367
                                                                                                                                                                                                                                                      YVP----GRDKPDLPT----WKRNFRSALNRKEGLRLAEDRSKDPHDPHKIYEFV---- 110
                                                                                                    -----DPGPP----SLAVAPEPCPO 169
                                                                                                                                                       223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  threonine; carboxy terminus; aspartic acid; mutant; phosphorylation; post-translational modification; sendai virus; cancer treatment; herpes; activator; promoter; PRDI/PRDIII; ISRE regulatory element; stimulation; DNA binding; transcriptional activity; transcriptional co-activator; CBP/p300; proteasome mediated degradation; viral infection; influenza; HIV infection; activate; cytokine gene; target cell:
                                                  -----TO
                                                                                                                                                                               SCTFLYGPPDPAVRATDPQQVAPPSPA-ELPDQKQLRYTEBLLRHVAPGLHLELRGPQLW
                                                                                                                                                                                                                                   ARRMGKCKVYWEVG------GPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFR
                                                                                                                                                                                                                                                                                       ARQRRGSPRYT1YLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDL
                                                                            190 SCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQ
                                                                                                                                               EGLRIVG-SEVGDRILPGWPVILPDPGMSLTDRGVMSYVRHVLSCLGGGLALWRAGQWLW
                        WREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interferon regulatory factor; IRF-3; transactivation domain; serine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replaced with Asp"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DAVI-) DAVIS-JEWISH GEN HOSPITAL MORTIMER B.
                                                  -NSGVG----DFSQPDTSPDTNGG-----
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DLHISNSHPLSLTSDQYKAYLQDL 415
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                                                                                                                                                                                                                                                                                                                                           DLCLSSANSL - - - YDDIECFLMEL
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY15102 standard; Protein; 427
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                                                                                                    EDILDELL-GNMVLAPLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 ARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDL 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSRELC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 WREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GSTSD-----TQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 EDILDELL-GNMVLAPLP------DPGPP-----SLAVAPEPCPO 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 EGLRLVG-SEVGDRTLPGWPVTLPDPGMSLTDRGVMSYVRHVLSCLGGGLALWRAGQWLW 282
                                                                                                                                                                                              The present protein sequence is the interferon regulatory factor-3 (IRF-3)5D protein, that is modified in the transactivation domain. The serine and threonine residues in the carboxy terminus are modified post-translationally, by phosphorylation, following sendai virus infection. The modified IRF-3 substituted with aspartic acid, functions as a strong activator of promoters containing PRDI/PRDII or ISRE regulatory elements, etimulation of DNA binding and transcriptional activity, association of IRF-3 with the transcriptional co-activator CBP/p300 and proteasome mediated degradation. The modified IRF proteins are used for the treatment of viral infections like, influenza, herpes or HIV infection. They may also be used to activate a cytokine gene, in cancer treatment or to modify a target cell of an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                           Carboxy-terminus modified highly active forms of interferon regulatory factor proteins used for the treatment of viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YVP----GRDKPDLPT-----WKRNFRSALNRKEGLRLAEDRSKDPHDPHKIYEFV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 SCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLRSPSLDNPTP-----FPNLGPSENPLKRLLVPGEEWEFEVTAFYRGRQVFQQTISCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCTFLYGPPDPAVRATDPQQVAFPSPA-ELPDQKQLRYTEELLRHVAPGLHLELRGPQLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 AQRIGHCHTYWAVSEBLLPNSGHGPDGE------VPKDKEGGVFDLGPFIVDLITFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 PRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.5%; Score 450; DB 20; I
27.8%; Pred. No. 8.6e-26;
tive 63; Mismatches 193;
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                                                                                                                                                                    Claim 8; Fig 10; 93pp; English
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                                                      WPI; 1999-620201/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     427 AA;
                                                                          N-PSDB; AAX90992
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us-09-647-965-9 1.rag

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393

(first entry)

22-AUG-2002

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Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; disorder; anodocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gestrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cycostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                         Human ovarian antigen HPDRA44, SEQ ID NO:4045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; SEQ ID No 4045; 2922pp; English.
                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                             07-JUN-2001; 2001WO-US18569.
                                                                                                                                                                                                                                                                                      07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                       neurological diseases -
                                                                                                                                                                                                                                                                                                                                    Birse CE, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-147878/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 AA;
                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABQ55990
                                                                                                                                                                                                              WO200200677-A1
                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                      03-JAN-2002
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RRGSPRY-TIY----LGFGQDLSAGRPKEK-----SLVLVKLEPWLCRVHLEGTQREG 469
                                                                                                                                                                                                                                                                                                        118 RHGAPWLPTLYHLPGLRAG-PVSLGGPRRRPGPGEAGTLVV------PMHLEGTHXK- 167
                                                                                                                                                    ----ELVEFRARQ 421
                                                                            2 PAXLPDQKQLRYTEELIRHVAPGLHLELRGPQXWARRMGKCKVYWEVGGPPGSASPSTPA 61
                                                                                                                                                                                 16 EWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS
                                               334 PAELPDQKQLRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPA
58; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel murine lymphocyte-specific interferon regulatory factor [LSIRF or ISF-3] (AAR99426) binds to interferon-stimulated response elements in DNA. Its amino acid sequence was deduced from a CDNA clone (AAT41701) isolated from a mouse spleen cDNA library. Recombinant LSIRF can be produced in transformed prokaryotic or eukaryotic host cells. LSIRF polypeptides are useful as targets for therapeutic cpds. used to regulate lymphocyte activation. By blocking LSIRF activity it is possible to suppress lymphocyte activation in response to certain environmental stimuli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New genes for murine lymphocyte specific interferon regulatory factor - used for modulation of lymphocyte activation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 450;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine lymphocyte specific interferon regulatory factor.
16;
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9; Mismatches
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                                                                                                                                                    394 CLLPRNCDTPIFDFRVFFQ
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95US-0422733.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          168 VGFLD 172
                                                                                                                                                                                                                                                                                                                                                          470 VSSLD 474
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Matches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens to polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigens polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders (e.g., infertility, disorders of pregnancy, anovulation, polyndrome, ovarian or press of pregnancy, anovulation, polystic ovary syndrome, ovarian cysts, and dysmenorrhoes), endocrine disorders, infertions (e.g., chamadial and acquired to disorders, infertions (e.g., chamadial and acquired vapinties), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, capinal disorders, and urinary system disorders of solvarian antigen systemic disorders of mol urinary system disorders. Ovarian respiratory doubless and polynucleotides may also be used in screening for compounds which further he used for game therapy, chromosome manning in the polynucleotides may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human overtian antigen of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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Pred. No. 6e-26;
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22;

74

16.3%; 55.1%;

Query Match Best Local Similarity

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AA;
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81
                                                                   -------vpegakkgakoltiddiqmamghpypmtap---ygsipaqqvhny
                RGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREG
                                                                                      CLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAG----GPGLP----AGELYGWAVE
                                                                                                                         TTPSPG-POPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTV
                                                                                                                                        ESOAPGI PIEPSIRSAEALA------LSDC------RLHICLYYRDILV
                                                                                                                                                            LQKVVGHP-SCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHL
                                                                                                                                                                            KELTTTSPEGCRISHG---HTYDVSNLDQVLFPYP---DDNGQRKNIEKLLSHLERGLVL
                                                                                                                                                                                              ELRGPQLWARRMGKCKVYWEVGGPPGSAS--PSTPACLLPRNCDTP1FDFRVFFQELVEF
OWLIDQIDSGKYPGLVWENEEKSVFRIPWKHAGKQDYNREEDAALFKAWALFKGKF----
                           /note= "the Double Q form of hLSIRF contains an additional glutamine residue between residues 163 and 164 of the Single Q form"
                                                                                                                                                                                                                                                                                                                                                                   Lymphocyte specific interferon regulatory factor; LSIRF; IRF-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes for murine lymphocyte specific interferon regulatory
                                                                                                                                                                                                                                          -AHHGRPAPRFOVTLCFGEEFPDPO-RORKLITAHVEPLLAR 411
                                                                                                                                                                                                                                RARORRGSPRYTIYLGFGODLSAGRPKEKSLVLVKLEPWLCR 459
                                                                                                                                                                                                                                                                                                                                                 Human lymphocyte specific interferon regulatory factor
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163..164
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                                                                                                                                                                                                                                                                                             standard; Protein; 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CANADA INC.
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N-PSDB; AAT41706.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LDRSW-RDYVPDQPHPEIPYQCPMTFGPRGHHWQGPACENGCQV-TGTFYACAP 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 PESQAPGVPTEPSIRSAEALA-------FSDC-----RLHICLYYREIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel Single Q or Double Q forms of human lymphocyte-specific interferon regulatory factor (LSIRF or ISF-3) (AAR99426) bind to interferon regulatory factor (LSIRF or ISF-3) (AAR99426) bind to interferon-etimulated response elements in DNA. The amino acid sequence of the Sigle Q form was deduced from a CDNA clone (AAT41706) isolated from a human lymphocyte CNNA library. Recombinant LSIRF can be produced in transformed prokaryotic or eukaryotic host cells. LSIRF polypeptides are useful as targets for therapeutic cyds. used to regulate lymphocyte activation. By blocking LSIRF activity it is possible to suppress lymphocyte activitation in response to certain environmental stimuli.
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rches 194;
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                                                                                                                                                                                                                                                                                                                                                                                                             13.2%; Score 361.5; 1
27.2%; Pred. No. 4.3e
ive 70; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 CLADHLLTASWGADPVPTKAPGEGQEGLPLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW38426 standard; Protein; 451 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLPEHISNPEDYHRSI
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 27.2
hes 135; Conservative
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Mon May

PEHISNPEDYHRSI 444

431

479 DLCLSSANSLYDDI 492

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(UYCO ) UNIV COLUMBIA NEW YORK 97WO-US09065. 96US-0654482. Dalla-Favera R; 28-MAY-1997; 28-MAY-1996;

WPI; 1998-032309/03. N-PSDB; AAV04017 Determining predisposition to multiple myeloma - allows identification of MUM-1 and MUM-2 genes, and determines specific chromosome 14 lesion

Claim 29; Fig 5B; 143pp; English

This protein is encoded by a candidate human proto-oncogene, MUM-1 (multiple myeloma oncogene 1) (see AAV04017). Juxaaposition of the MUM-1 gene to the IgH gene as a result of t(6;14) (p25;932) translocation is recurrent in multiple myeloma (MM). The invention provides: a method of determining a chromosomal breakpoint in a subject suffering from MM, a method of identifying a gene located in chromosome 14 that is altered by a chromosomal breakpoint detected in a subject suffering from MM; a nucleic acid probe; a method for detecting a predisposition to MM, a nucleic acid probe; a method for capable of hybridising to m RNM or CDNA encoding a MUM protein; and a pharmaceutical composition comprising an oligonucleotide effective in preventing overexpression of a MUM protein. Analysis of 144-chromosomal translocations and identification of genes altered in MW will allow: (1) the determination of chromosomal sequences lesion 144+ translocations, the most important cytogenetic lesion associated with MM pathogenesis elucidation; (2) elucidation of specific gene lesions for MM; (3) a diagnostic method based on counteracting the action of abnormal gene products. 

451 AA; Sequence

Gaps 92; DB 19; Length 451; 13.1%; Score 357; DB 19; Length 45 27.3%; Pred. No. 9.3e-19; ive 73; Mismatches 194; Indels Local Similarity 27.3 nes 135; Conservative Query Match Best Local S Matches 135

EWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS 56 16

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ARORRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDL 478 .. <u>:</u> <u>:</u> --419

361 LRGPQLWARRMGKCKVYWEVGGPPGSAS--PSTPACLLPRNCDTPIFDFRVFFQELVEFR 418

Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; hinhibin; ohemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; oconary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytosteatic; osteopathic; vascucpic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer. Human IFN regulatory factor 7 homologue, SEQ ID NO:1410. ABB11040 standard; peptide; 72 AA. 11-JAN-2002 (first entry) ABB11040; 

WO200157188-A2.

09-AUG-2001

05-FEB-2001; 2001WO-US03800.

03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

HYSE-) HYSEQ INC.

Drmanac RT; Liu C, Tang YT,

2001-457740/49. N-PSDB; ABA08284. Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -

Claim 20; Page 139; 1963pp; English.

242

193 ADHLLTASWGADPVPTKAPGEGOEGLPLT-----GACAGGPGLPAGELYGWAVET

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of identifying compounds which bind to polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention have homology to known proteins, thereby polypeptides of the invention have homology to known proteins, thereby polypeptides of the invention have homology to known proteins, thereby polypeptides of the invention have homology to known proteins, thereby polymential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; inmunomodulatory activity; tissue growth activity; immunomodulatory activity; tissue growth activity; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or limbin-related activities; chemotactic or chemokinetic activities; no may be involved in oncogenesis, cancer cell proliferation or metastasis.

Depending on their biological activities, polypeptides and nucleotides of

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that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug
   invention are useful for preventing, treating or ameliorating medical
                   conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthmia or arthritis), proliferative retinopathy, atherosclerosis; coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening techniques. The present sequence represents a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide of the invention.
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72 AA; Sequence

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1 GGPPGPFLAHTHAGLQAPGPLAPAGDEGDLLLLAVQQSCLADHLLTASWGGKDPIPTKA 60
                                                              GGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQSCLADHLLTASWGA-DPVPTKA
                              4; Indels 1;
   Length 72;
Score 335.5; DB 22;
Pred. No. 4.4e-18;
                              2; Mismatches
 12.3%;
90.1%;
                                 64; Conservative
                                                                                                                         211 PGEGQEGLPLT 221
                                                                                                                                                       61 LGEGQEGLPLT 71
                 Best Local Similarity
   Query Match
                                 Matches
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210

ABB11963 standard; peptide; 392 AA.

ABB11963;

11-JAN-2002 (first entry)

Human IFN regulatory factor homologue, SEQ ID NO:2333.

Human, cytokine; cell proliferation, cell differentiation, growth factor, haematopoiesis regulation, tissue growth, immunomodulator, activin, haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemckaris; chemckinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; els cutture; drug screening; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiachmatic; antiarthitic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vascuropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer 

Homo sapiens

WO200157188-A2

09-AUG-2001.

03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

05-FEB-2001; 2001WO-US03800.

(HYSE-) HYSEQ INC.

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Drmanac RT; Liu C, Tang YT,

2001-457740/49. N-PSDB; ABA09207 

oteins and DNA encoding sequences useful for preventing, or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -Human proteins treating or ame

Claim 20; Page 287-288; 1963pp; English

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a comprise and as relates to vectors and recombinant host cells comprising a comprise the invention. Although novel polypeptides, and the invention and sethods of detecting the nucleotides or polypeptides of the invention. Although novel, many of the bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention. The polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence conferenced in the sequence activities, and hence differentiation activities, including cytokine, cell proliferation or cell differentiation activities, including cytokine, cell proliferation or cell conferenced or conferenced activities; the membropolytic activities; seem cell growth activity; issue growth activity; involved in oncogenesis, receptor or ligand activities, or may be conferenced on the invention are useful for preventing, treating or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include arterial isonemia, bone disorders (e.g., method or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), corditions, e.g., by protein or gene therapy. Such conditions include retrial isonemia, bone disorders (e.g., method or lymphoid cell disorders) carde encoding them) may be used to promote wound repair (or nucleic acide encoding them) may be used to promote cells includes may be used in cellmunomedulatory activities may be used in the treatment of viral, chart can be used to augment or remained the conditions includes and publications in adjutton to immune disorders (e.g., promote cells in culture to give rise to neurosphinal activity may be used in cell and burged to augment or seman that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides any also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.

392 AA; Sequence

19; 175 FQCTISCPEGLRLVG-SEVGDRTLPGWPVTLPDPGMSLTDRGVMSYVRHVLSCLGGGLAL 233 62 AWAVARGRWPPSSRGGCPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKV 121 122 YALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGD 181 182 LLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVE 241 94 -----TQEDILDELL-GNMVLAPLP------SLA 120 242 TIPSPGPOPAALITGEAAAPESPHQAEPYLSPSPSACTAVQEP-SPGALDVTIMYKGRIV 300 174 301 LOKVVGHPSCTFLYGPPDPAVRATDPQQVAFPSPA-ELPDQKQLRYTEELLRHVAPGLHL 359 65 93 66 YEFV----NSGVG----DFSQPDTSPDTNGG-----GSTSD 15 AWAEATGAYVP----GRDKPDLPT----WKRNFRSALNRKEGLRLAEDRSKDPHDPHKI 11.7%; Score 320; DB 22; Length 392; 26.0%; Pred. No. 4.8e-16; .ive 51; Mismatches 176; Indels 112; Gaps Matches 119; Conservative Query Match Best Local Similarity

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------DPGPP----SLA 120
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                                                                                                                                                                62 AWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKV 121
                                                                                                                                                                                                                                                   122 YALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGD 181
                                                                                                                                                                                                                                                                                                                                   182 LLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 F-----QELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 IVGSLGPPDLITFTEGSGR-SPRYALWFCVGESWPQDQPWTKRLVMVKVVPTCLRALVEM 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 PQQTISCPEGLRLVG-SEVGDRTLPGWPVTLPDPGMSLTDRGVMSYVRHVLSCLGGGLAL
                                                                                                                                                                                        ---GSTSD
                                                                                                                                                                                                                                                                                                                                                                                                                     242 TTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEP-SPGALDVTIMYKGRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 LOKVVGHPSCTFLYGPPDPAVRATDPQQVAFPSPA-ELPDQKQLRYTEELLRHVAPGLHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 ELRGPQLWARRMGKCKVYWEVG-----GPPGSASPSTPACLLPRNCDTPIFDFRVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 WRAGOWLWAORLGHCHTYWAVSEELLPNSGHGPDGE------VPKDKEGGVFDLGPF
                                                                                                                         Gaps
                                                                                                                       Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      brain tissue;
seizure;
                                                                                  DB 22; Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein encoded by gene 55 clone HPRCU93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 ARVGGASSLENT-VDLHISNSHPLSLTSDQYKAYLQDL 380
                                                                                11.7%; Score 320; DB 22; 26.0%; Pred. No. 4.8e-16; ive 51; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; testis; tumour; foetal fusion protein; cancer; central nervous system; diagnosis; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         465 TQREGVSSLDSSDLDLCLSSANSL---YDDIECFLMEL
                                                                                                                                                                                                                                                                                                                                                                          -----TÓEDILĎEĽĽ-GNMVLAPLP-----
                                                                                                                                                                                                                                                                                          66 ÝEFV----NSGVG----DFSQPDTSPDTNGG-
of publication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW74784 standard; Protein; 373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373
label= unknown
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97US-0038621.
97US-0040161.
97US-0040162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                   Local Similarity 26.0
  time
were missing at the
                                         392 AA;
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07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                              94
                                           Sequence
                                                                                Query Match
                                                                                                                         Matches
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SXS
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                       410
                                                                                                   F-----QELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEG 464
                                                                                                                                          285 IVGSLGPPDLITFTEGSGR-SPRYALWFCVGESWPQDQPWTKRLVMVKVVPTCLRALVEM 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment of cancer, leukaemia, nervous system disorders, arthritis and
inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
                                           234 WRAGQWLWAQRLGHCHTYWAVSEELLPNSGHGPDGE-----VPKDKEGGVFDLGPF
                     ----GPPGSASPSTPACLLPRNCDTPIFDFRVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides with cytokine-like activities,
useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Cao Y,
Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ж
к,
                                                                                                                                                                                                            344 ARVGGASSLENT-VDLHISNSHPLSLTSDQYKAYLODL 380
                                                                                                                                                                                      TOREGVSSLDSSDLDLCLSSANSL---YDDIECFLMEL 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C, Drmanac RT, Asundi V, Zhou P,
Wang D, Wang J, Zhang J, Ren F, Chen
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 397; 6221pp; English.
                   ELRGPQLWARRMGKCKVYWEVG--
                                                                                                                                                                                                                                                                                                                                   AAM79970 standard; Protein; 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-05660875.
20-JUM-2000; 2000US-0598075.
19-JUM-2000; 2000US-0620325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0663561.
20-OCT-2000; 2000US-063325.
30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein SEQ ID NO 3616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                   360
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Zhao QA,
                                                                                                   411
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359

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970S-0040163.
970S-0040333.
970S-0040333.
970S-00403312.
970S-0043312.
970S-0043313.
970S-0043313.
970S-0043313.
970S-0043569.
970S-0043569.
970S-0043569.
970S-0043569.
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97US-0048974.
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970S-0055724
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9703-0056872.
9703-0056874.
9703-0056875.
9703-0056876.
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23-MAY-1997;
23-MAY-1997;
                                                                11-APR-1997;
11-APR-1997;
11-APR-1997;
                                                                                                                                       23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
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22-AUG-1997;
                                                    11-APR-1997;
                                                                                                                                  23-MAY-1997,
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23-MAY-1997
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08-JUL-1997
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                          07-MAR-1997
11-APR-1997
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                                                                                                                           23-MAY-1997
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This sequence represents a secreted human protein encoded by the nucleic acid molecule designated Gene 54 from the human cDNA clone HPRCU93

Cdeposited as clone ATCC 97899 and ATCC 209045).

The gene can be used to generate fusion proteins by linking to the gene con be used to generate fusion proteins by linking to the gene con a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812, amino acid sequences AAW4731-W75026)

Which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides in a sample or by determining the presence of mutations in the new polynucleotides. Described uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                 DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA; Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS; Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA; Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 573-574; 721pp; English.
                          970S-0056881
970S-0056881
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                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-506364/43.
N-PSDB; AAV59565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 373 AA;
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                                                           22-AUG-1997;
                                                                                                                                                                                                                                                               22-AUG-1997;
22-AUG-1997;
05-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Feng P,
Kyaw H,
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115 PADPHKVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPA 174

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Query Match
9.5%; Score 259.5; DB 19; Length 373;
Best Local Similarity 25.2%; Pred. No. 1.6e-11;
Matches 100; Conservative 59; Mismatches 165; Indels 73;

73; Gaps

PWNPVKIY----QVC-----DIPQPQG------SIINPGSTGS 36

175 PAGDKGDLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPL----TGACAGGPGL 230

37 APWDEKD----NDVDEEDEEDE-LDQSQHHVPIQDTFPFLNINGSPMAPASVGNCSVGNCS

231 PAGELYGWAVETTPSPGPOPAALTTGEAAAPESPHOAEPYLSPSPSACTAVQEPSPGALD 290 PEAV---W------PKTEPLEMEVPQ--APIQPFYSSPELMISSLPMT-----DLD 132

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Human, S' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a polypeptide encoded by one of a large number of 5. ESTs derived from mRNAs encoding secreted proteins. The 5. ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3. untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5. ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5. UTR is rarely included. 5. ESTs are derived from mRNAs with intact 5. ends and can therefore be used to obtain full length cDNAs and genomic DNARs. 5. ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 136;
| : | | | : | : | : | : | EMFSGDFTRSFDSGSVRLQISTPD-IKDNIVAQLKQL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
7.8%; Score 214; DB 21;
Best Local Similarity 36.3%; Pred. No. 1.3e-08;
Matches 45; Conservative 21; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; SEQ ID 5424; 71pp + CD-ROM; English
                                                                                                                                                                                                                        Human secreted protein, SEQ ID NO: 5424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duclert A,
                                                                                                         AAG01343 standard; Protein; 136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2000; 2000EP-0200610.
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N-PSDB; AAC01349.
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                                                                                                                                                                                                                                                                                                                  Homo sapiens
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46; Indels 12;

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70 ----KEGDTGGPAVWKTRLRCALNKSSEPKEVPERGRMDVAEPYKVYQLLPXGIVSXQP 124
                                                                   76 GGGPPPEABTAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREGP 134
17 WLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSE-ADARIFKAWAVARGRWPPSSR 75
                  completed: June 18, 2003, 12:46:45
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PIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHL 462

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133 IKFQYRGKEYGÓTWTVSNÞQGCRLFYGDLGÞMPDQEELFGPVXLEQVKFÞGÞEHITNEKÓ 192

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291 VTIMYKGRTVLQKV-VGHP-SCTFLYGPPDPAVRATD-----PQQVAFPSPAELPDQKQ 342

343 LRYTEELLRHVAPGLHLELRGPOLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDT 402

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Query Match
Best Local Similarity
Matches 498; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 374,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 52,
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2731
1 MALAPERAAPRVLFGEWLLG......SANSLYDDIECFLMELEQPA
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US-08-705-771-16
US-08-611-280-2
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US-09-230-371A-29
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PCT-US91-06532-3
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993
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seq length: 200000000
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APPLICANT: Gish, Kurt C.
APPLICANT: Sequent C.
APPLICANT: Sequezat, Wolfgang
APPLICANT: Shanaban, Frances
APPLICANT: Shanaban, Frances
APPLICANT: Lees, Emma M.
APPLICANT: Lees, Emma M.
APPLICANT: Lees, Emma M.
APPLICANT: McClanaban, Terrill K.
TITLE OF INVENTION: Intracellular Regulatory Molecules;
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES:
ADRESSE: DNAX Research Institute
CITY: Palo Alto
STREET: 901 California Avenue
CITY: Palo Alto
STREET: 901 California Avenue
CITY: Palo Alto
STREET: 904 California Avenue
CITY: Palo Alto
STREET: 904 California
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US 60/032,818
FILING DATE: 10-DEC-1997
CLASSIFICATION NUMBER: US 60/032,818
FILING DATE: 11-PERC-1996
ATTORNEY AGENT INFORMATION:
NAME: Ching, Edwin P.
REBERENCE/DOCKET NUMBER: DX0646
TELERDHOMALCATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.7%; Score 2695; DB 4; Length 503; 99.0%; Pred. No. 3e-223; Live 0; Mismatches 5; Indele
                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08999774A Patent No. 6274312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 503 amino acids
amino acid
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MOLECULE TYPE: protein
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19;

Gaps

63

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130 WREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 SCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.7 EDILÜELL-GNMVLAPLP-------DPGPP-----SLAVAPEPCPO 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 PAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEP-SPGALDVŢIMYKGRTVLQKVVGHP 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 EGLRLVG-SEVGDRTLPGWPVTLPDPGMSLTDRGVMSYVRHVLSCLGGGLALWRAGOWLW 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 ARRMGKCKVYWEVG-----GPPGSASPSTPACLLPRNCDTPIFDFRVFFOELVEFR 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 -NSGVG----DFSQPDTSPDTNGG-----TQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 PLRSPSLDNPTP-----FPNLGPSENPLKRLLVPGEEWEFEVTAFYRGRQVFQQTISCP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 AQRLGHCHTYWAVSEELLPNSGHGPDGE------VPKDKEGGVFDLGPFIVDLITFT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 ARORRGSPRYTIYLGFGODLSAGRPKEKSLVLVKLEPWLCRVHLEGTOREGVSSLDSSDL 478
                                                                                                                                                                                                                                                                6 PRXL--PWLVSQLDLGQLEGVAWVNKSRTRFRIPWKHGLRQDAQQEDFGIFQAWAEATGA
                                                                                                                                                                                                                                       10 PRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVARGR
                                                                                                                                                                                                                                                                                                                                                                      64 YVP----GRDKPDLPT----WKRNFRSALNRKEGLRLAEDRSKDPHDPHKIYEFV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 SCTFLYGPPDPAVRATDPQQVAFPSPA-ELPDQKQLRYTEELLRHVAPGLHLELRGPQLW
                                                                                                                                                   Query Match 16.6%; Score 454; DB 3; Length 427;
Best Local Similarity 28.0%; Pred. No. 4.8e-31;
Matches 141; Conservative 63; Mismatches 192; Indels 108;
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Patent No. 589166

GENERAL INFORMATION:
APPLICANT: Matsuyama, Toshifumi
APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: INC. Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 APPLICATION DATA:
APPLICATION NUMBER: US/08/611,280 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6733 Mississauga Road, Suite CITY: Mississauga STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392 DLHISNSHPLSLTSDQYKAYLQDL 415
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                    427 amino acids
SEQUENCE CHARACTERISTICS
                                                                             , MOLECULE TYPE: protein US-08-705-771-16
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COMPUTER READABLE FORM:
                                      TYPE: amino acid
TOPOLOGY: linear
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: Canada
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                      LENGTH:
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                                                                                                                                 VYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGFFLAHTHAGLQAPGPLPAPAGDKG 180
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                                                                                                        KAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHK 120
                                                                                                                                                                                                                                     121 VYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPRPFLAHTPAGLQAPGPLPAPAGKG 180
                                             MALAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIF
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FILING DATE: August 30, 1996
CLASSIFACATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
RECISTRATION NUMBER: 33,073
REPERENCE/DOCKET NUMBER: 325800-346 (PF196)
TELEPHONE: 973-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/08705771
Patent No. 6054289
GENERAL INFORMATION:
APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
APPLICANT: Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
TITLE OF INVENTION: Expression Products
NUMBER OF SEQUENCES: 22
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ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
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COMPUTER READABLE FORM:
MEDLUM TYPE: 3.5 INCH DISKETTE
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OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
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INFORMATION FOR SEQ ID NO: 16:
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STATE: NEW JERSEY
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US-08-705-771-16
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us-09-647-965-9 1.rai

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CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                              CLASSIFICATION:
                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                          FILING DATE:
                               FILING DATE
                                                                                                                                                                                                                                          TOPOLOGY:
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US-09-562-466-2
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                                                                                                                                                                                             LENGTH:
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Patent No. 6258935
GENERAL INFORMATION:
APPLICANT: Mateuyama, Toshifumi
APPLICANT: Grossman, Alex
APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                             Length 450;
                                                                                                                                                                                                         13.8%; Score 376; DB 2; Length 45 28.1%; Pred. No. 2.5e-24; Ative 66; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCR 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATE: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
CITY: Mississauga
                                                           A-338A
                             NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-3
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                      LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                , MOLECULE TYPE: protein US-08-611-280-2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                   linear
                                                                                                                                                                                                                           Similarity
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COUNTRY:
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US-09-195-940-2
                                                                                                    LENGTH:
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Best Local S
Matches 130
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128 -------YGSLPAQVHNY 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 ESQAPGIPIEPSIRSAEALA------LSDC------RLHICLYYRDILV 263
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TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Canada Inc.
STREET: 673 Mississauga Road, Suite 303
CITY: Mississauga
STATE. Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 450;
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28.1%; Pred. No. 2.5e-24;
tive 66; Mismatches 172; Indels
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US/09/195,940
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Patent No. 6369202
GENERAL INFORMATION:
APPLICANT: Matsuyama, Toshifumi
                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/611,280
                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               450 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  single
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELRGPQLWARRMGKCKVYWEVGGPPGSAS--PSTPACLLPRNCDTPIFDFRVFFQELVEF 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.8%; Score 376; DB 4; Length 450
Best Local Similarity 28.1%; Pred. No. 2.5e-24;
Matches 130; Conservative 66; Mismatches 172; Indels
                                              COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/562,466
FILING DATE: OT-MAy-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RARORRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCR 459
                                                                                                                                                                                     APPLICATION NUMBER: 09/195,940
FILING DATE: UDKNOWN>
ATTORIEY/AGENI INFORMATION:
NAME: 0leski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERRENCE/DOCKET NUMBER: A-338A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE_CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/08611280 Patent No. 5891666 GENERAL INFORMATION:
APPLICANT: Matsuyama, Toshifumi
                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                              LENGTH: 450 amino acids
                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
ZIP: L5N 6JB
COMPUTER READABLE FORM:
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310 F-AHHGRSLPRFQVILCFGEEFPDPQ-RQRKLITAHVEPLLARQLYYFAQQNSGHFLRGY 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 PGTDQTEAEAP--AAVPPPQGGPPGPFL-AHTHAGLQAPGPLPAPAGDKGDLLLQAVQQS 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97;
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                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.2%; Score 361.5; DB 2; 27.2%; Pred. No. 4.4e-23; iive 70; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 -GAKÓLTLEDPOMSMSHPYTMTTPYPSLPAQVHNYMMPP-
                   3: Amgen Canada Inc.
6733 Mississauga Road, Suite 303
                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-3
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLPEHISNPEDYHRSI 443
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                                                                                                                                                                                   Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                              ZIP: L5N 6JB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-611-280-25
CORRESPONDENCE ADDRESS
                                                                 Mississauga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                         Ontario
: Canada
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les 135; Conserv
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                                                                                                                                                                                   MEDIUM TYPE:
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                 ADDRESSEE:
                                                                                                               COUNTRY:
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Matches
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RESULT 7 US-09-195-940-25

APPLICANT: Grossman, Alex APPLICANT: Richardson, Christopher D. TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES

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82 REGIDKPDPPT-----WKTRLRCALNKSNDFEELVERSQLDISDPYKVYRIVPEGAKK-- 134
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75 RGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREG 133
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                                                                                                                                                                                                                                                                                                                                     Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%; Score 361.5; DB 4;
27.2%; Pred. No. 4.4e-23;
tive 70; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
CITY: Mississauga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/562,466
FILING DATE: 01-May-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-338A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/195,940
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                              APPLICANT: Matsuyama, Toshifumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Ontario
COUNTRY: Canada
ZIP: LSN 6JB
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                       Sequence 25, Application US/09562466 Patent No. 6369202 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 450 amino acids
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                                                                         492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                         477 DLDLCLSSANSLYDDI
                                                                                                                      428 DLPEHISNPEDYHRSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.2
Best Local Similarity 27.2
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino
                                                                                                                                                                                                              US-09-562-466-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-562-466-25
                             370
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                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 CLADHLLTASWGADPVPTKAPGEGQEGLPLT-----GACAGGPGLPAGELYGWAV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ETTPSPG-PQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 VLOKVVGHP-SCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLH 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 VKELTTSSPEGCRISHG---HTYDASNLDQVLFPYP---EDNGQRKNIEKLLSHLERGVV 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 LELRGPQLWARRMGKCKVYWEVGGPPGSAS--PSTPACLLPRNCDTPIFDFRVFFQELVE 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 FRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSS 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 RGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | : : |:
|-----FSDC------RLHICLYYREIL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 -GAKÖLTLEDPOMSMSHPYTMTTPYPSLPÄQVHNYMMPP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 QWLIDQIDSGKYPGLVWENEEKSIFRIPWKHAGKQDYNREEDAALFKAWALFKGKF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LDRSW-RDYVPDQPHPEIPYQCPMTFGPRGHHWQGPACENGCQV-TGTFYACAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 EWLLGEISSGCYECLQWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.2%; Score 361.5; DB 4; Length 450; 27.2%; Pred. No. 4.4e-23; ive 70; Mismatches 194; Indels 97
                                                                  APPLICANT: Matsuyama, Toshifumi
APPLICANT: Matsuyama, Toshifumi
APPLICANT: Grossman, Alex
APPLICANT: Grossman, Alex
APPLICANT: Grossman, Alex
APPLICANT: Movel Genes D.
ALTILE OF INVENTION: 25
CORRESPONDENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEB: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
CITY: Mississauga
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/195,940
                                                                                                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/611,280
  Sequence 25, Application US/09195940
Patent No. 6258935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34,688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 450 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 27.2°
Matches 135; Conservative
                                                                                                                                                                                                                                                                                   ZIP: L5N GUB
ZIP: L5N GUB
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-195-940-25
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74 81

Gaps

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APPLICANT: CHANG, TAGEN
APPLICANT: Bohenzky, Roy A
APPLICANT: Russo, James J
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 45185-6-PCT-US
CURRENT PAPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1997-11-17
PRIOR FILING DATE: 1997-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254
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                                                                                                                                                 76 GGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREGP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 GTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQSCLAD 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------AMONCTLSP 156
--- QQVHNYMM 171
                                                                               172 PP--LDRSW-RDYVPDQPHPEIPYQCPMTFGPRGHHWQGPACENGCQV-TGTFYACAPPE 227
                                                                                                                          243 TPSPG-PQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVL 301
                                                                                                                                                                                                       302 OKVVGHP-SCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTBELLRHVAPGLHLE 360
                                                                                                                                                                                                                                             265 ELTTSSPEGCRISHG----HTYDASNLDOVLFPYPEDNGHRKNI----ENLLSHLERGVVLW 318
                                                                                                                                                                                                                                                                                        361 LRGPQLWARRMGKCKVYWEVGGPPGSAS--PSTPACLLPRNCDTPIFDFRVFFQELVEFR 418
                                                                                                                                                                                                                                                                                                                                                                     419 ARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDL 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 WLLGEISSGCYEGLQWLDEARTCPRVPWKHFARKDLSE-ADARIFKAWAVARGRWPPSSR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GACAGGPGLPAGELYGWAVET
                                                                                                                                                                                                                                                                                                                            319 MAPDGLYAKRLCQSTIYWD--GPLALCNDRPNK----LERDQTCKLFDTQQFLSELQAF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 WVVEQVESGOFPGVCWDDTAKTMFRIPWKHAGKQDFREDQDAAFFKAWAIFKGKY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 HILTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQPAALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
  --SMSHPYT-MTTPYPSLPA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 328.5; DB 4;
; Pred. No. 2.5e-20;
69; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 SVLQDSLNNEE-----EGASG----GAVHSDIG----
                                          193 ADHLLTASWGADPVPTKAPGEGQEGLPLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/09230371A Patent No. 6348586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.0%;
25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         479 DLCLSSANSLYDDI 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               431 PEHISNPEDYHRSI 444
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SOFTWARE: Patentin Ver. 2.0
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  135 -GAKQLTLEDPQM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 ĠŤQKVPSK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Chang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-230-371A-29
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LENGTH: 393
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                                                                                                                                                   RGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 PGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGP-LPAPAGDKGDLLLQAVQQSCL 192
                                        VLQKVVGHP-SCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLH 358
                                                                                 262 VKELTTSSPEGCRISHG---HTYDASNLDQVLFPYP---EDNGQRKNIEKLLSHLERGVV 315
                                                                                                                                                                                                           FRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSS 476
  --FSDC------RLHICLYYREIL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73; Mismatches 194; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08654482
Patent No. 6245562
GENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
TITLE OF INVENTION: IDENTIFICATION OF GENES ALTERED IN
TITLE OF INVENTION: MUTIFILE MYELOMA
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILICATION NUMBER: US/08/654,482
FILING DATE: 28-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 357; DB 4;
Pred. No. 1.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  225 PESQAPGVPTEPSIRSAEALA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 5095
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INPOMMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                          DLDLCLSSANSLYDDI 492
                                                                                                                                                                                                                                                                                                                                 DLPEHISNPEDYHRSI 443
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27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451 amino acids
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Best Local Similarity 27.3<sup>3</sup>
Matches 135, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-654-482-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
COUNTRY: U.S.A.
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,596
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/040,163
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APPLICATION NUMBER: 60/047,615
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,617
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APPLICATION NUMBER: 60/047,503
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APPLICATION NUMBER: 60/047,581
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                                                                                                                                                                                                                                                  Sequence 374, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
                                                                                               464 GTQREGVSSLDSSDL------
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TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND TITLE OF INVENTION: USES THEREOF FILE REPERENCE: 45185-G-PCT-US CURRENT APPLICATION NUMBER: US/09/230,371A CURRENT FILING DATE: 1999-11-17 PRIOR APPLICATION NUMBER: PCT/US97/13346 PRIOR PILING DATE: 1997-07-22 NUMBER OF SEQ ID NOS: 30
349
                                                                     310 CTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQLWAR 369
                                                                                                                                                              370 RMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRG-SPRY 428
                                                                                                                                                                                          292 RLCPIPISWNAPQAPPGPGPH----LLPSNECVELFRTAYFCRDLV--RYFQGLGPPPKF 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 -----KEGDKAEPATWKTRLRCALNKSPDFEEVTDRSQLDISEPYKVYRIVPEEDQKCK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 -----CWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGD 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 LLLOAVQOSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVE 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SQMVISFYYGGKLVG 217
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                                                                                                                  241 CRLV---AEPSGSESSMEQVLFPKPGPLEP-----TORLLSQLERGILVASNPRGLFVQ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----WAHE 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 EWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS
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                                                                                                                                                                                                                                                                           346 QVTLNFWEESHGSSHTPQNLITVKMEQAFARYLLEQTPEQQAAILSL 392
                                                                                                                                                                                                                                                    TIYLGFGODLSAGRPKEKSLVLVKLEPWLCRVHLEGT--OREGVSSL 473
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197 T-----EAPFQGDQRSLEFLLP-
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Edelman, Isidore S
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Bohenzky, Roy A
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Matches 123; Conservative
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ORGANISM: Human
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US-09-230-371A-30
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404 IFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLE 463
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                                                                                                                                                                                                                              375 QLAEEAGKSCGAGSVMQAPEEPPPDQVFRMFPDICASHQRSFF 417
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TITLE OF INVENTION: 186 Human Secreted proteins
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FLING DATE: 1998-03-06
APPLICATION NUMBER: 60/040,162
FILING DATE: 1997-03-07
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R APPLICATION NUMBER: 60/043,672
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,315
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,974
R APPLICATION NUMBER: 60/056,886
R FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                        R APPLICATION NUMBER: 60/043,671
R FILING DATE: 1997-04-11
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,669
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,312
R FILING DATE: 1997-04-11
R FILING DATE: 1997-04-11
R FILING DATE: 1997-04-11
                                                                    R APPLICATION NUMBER: 60/047,601
RR FILING DATE: 1997-05-23
RR APPLICATION NUMBER: 60/043,580
RR FILING DATE: 1997-04-11
RR APPLICATION NUMBER: 60/043,568
RR FILING DATE: 1997-04-11
RR APPLICATION NUMBER: 60/043,314
RR FILING DATE: 1997-04-11
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RR FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/056,903
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APPLICATION NUMBER: 60/056,888
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,911
 APPLICATION NUMBER: 60/047,612
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APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11
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PPLICATION NUMBER: 60/056,893
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PLICATION NUMBER: 60/056,630
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,882
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APPLICATION NUMBER: 60/056,637
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FILING DATE: 1997-08-22
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BARLIER F
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EARLIER APPLICATION NUMBER: 60/056,895
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,761
EARLIER APPLICATION NUMBER: 60/047,761
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-06-23
EARLIER FILING DATE: 1997-06-22
EA

Query Match 9.5%; Score 259.5; DB 4; Length 373; Best Local Similarity 25.2%; Pred. No. 2e-14; Matches 100; Conservative 59; Mismatches 165; Indels 73; Gaps

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16 EWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS 74
4 QWLIEQIDSSMYPGLIWENEEKSMFRIPWKHAGKQDYNQEVDASIFKAWAVFKGKF---- 59
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                                                                   75 RGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRE 127
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APPLICANT: Dalla-Favera, Riccardo
TITLE OF INVENTION: IDENTIFICATION OF GENES ALTERED IN
TITLE OF INVENTION: MULTIPLE MYELOMA
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSED: COOPER & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
TITLE OF INVENTION: IDENTIFICATION OF GENES ALTERED IN
TITLE OF INVENTION: MULTIPLE MYELOMA
TITLE OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: COOPER & Dunham LLP
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11.2%; Pred. No. 5.6e-12;
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STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6245562
                                                                                                                                                                                          Sequence 1, Application US/08654482
Patent No. 6245562
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TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 47; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-654-482-2
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                                                                                                         290
                                                                                                                                                                                                                          343 LRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDT 402
                                                                                                                                                                                                                                                                                                           403 PIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHL 462
                                                                                                                                                                                                                                                                                                                                                                                                 93 PEAV---W------PKTEPLEMEVPQ--APIQPFYSSPELWISSLPMT------DLD 132
                                                                                                                                                                                               291 VTIMYKGRTVLQKV-VGHP-SCTFLYGPPDPAVRATD-----PQQVAFPSPAELPDQKQ 342
                                                               37 APWDEKD---NDVDEEDEEDE-LDQSQHHVPIQDTFPFLNINGSPMAPASVGNCSVGNCS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 EWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS 74
                                                                                                         231 PAGELYGWAVETTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08654482
Patent No. 6245562
GENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
TITLE OF INVENTION: IDENTIFICATION OF GENES ALTERED IN
TITLE OF INVENTION: MULTIPLE MYELOMA
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           463 EGTQREGVSSLDSSDLDLCLSSANSLYDDIECFLMEL 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 EMFSGDFTRSFDSGSVRLQISTPD-IKDNIVAQLKQL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/654,482
FILING DATE: 28-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.3%; Score 228; DB 4; Best Local Similarity 41.2%; Pred. No. 1.9e-12; Matches 47; Conservative 20; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5099;
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (212) 278-0400
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS LENGTH: 107 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide US-08-654-482-5
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STRANDEDNESS: si
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U.S.A.
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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COMPUTER: TOUGH

MEDIUM TYPE: Floppy disk

COMPUTER: TEMP FC compatible

COMPUTER: TEM FC compatible

COMPUTER: TEM FC compatible

COMPUTER: TEM FC compatible

COMPUTER: TEM FC COMPUTER: TYPE: TEM FC COMPUTER: TY
                                                      New York
: U.S.A.
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16 EWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS 74 4 QWLIDQIDSGKYPGLVWENEEKSVPRIPWKHAGKQDYNREEDAALFKAWALFKGKF----8.1%; Score 222.5; DB 4; Length 108; 41.2%; Pred. No. 5.6e-12; tive 21; Mismatches 35; Indels 11; Gaps Query Match
Best Local Similarity 41.2\*
Matches 47; Conservative

Search completed: June 18, 2003, 12:48:51 Job time : 29 secs

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June 18, 2003, 12:47:53 ; Search time 50 Seconds (without alignments) 1088.561 Million cell updates/sec
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2731
1 MALAPERAAPRULFGEWLLG......SANSLYDDIECFLMELEQPA
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Compugen Ltd.
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version 5
- 2003 C
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
GenCore (c) 1993
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seq length: 200000000
                                              Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB
Maximum DB
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distribution.	Description	Sequence 2, Appli Sequence 374, App Sequence 14, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl	7, Ap 23, Ap 1159, Ap 22, Ap 22, Ap 1166, Ap 1128, Ap	
of the total score	SUMMARIES	US-09-975-253-2 US-09-99-391-374 US-09-893-519A-14 US-09-919-497-76 US-09-976-740-47 US-10-023-529-47 US-10-023-523-47	US-10-162-223-7 US-09-813-398-23 US-10-122-805-4 US-10-060-036-159 US-10-171-311-36 US-10-171-311-36 US-10-149-152-2 US-10-060-036-166 US-10-060-036-168 US-10-050-882-68 US-10-050-882-137 US-10-260-715-8	
sis	DB	122		
by analysis	% Query Match Length	427 373 1023 349 550 550 550	111. 125. 146. 146. 146. 146. 146. 146. 146. 146	
is derived b	% Query Match	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	លេលលលលលលលលល ង្នែក្នុងក្នុយល់ប្រហ	
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190 SCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQ

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Sequence 2, Appli Sequence 10, Appl Sequence 43, Appl Sequence 43, Appl Sequence 44, Appl Sequence 44, Appl Sequence 14, Appl Sequence 1, Appl Sequence 16, App Sequence 216, App Sequence 2, Appli Sequence 103, Appl Sequence 103, Appl Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 2, Appli	r Treating and Preventing Infection ulatory Factor 3 r Val	9; Length 427; 21; 192; Indels 108; Gaps 19;	PRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVARGR 69 	SRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDFADPHKVYALSRELC 129 	WREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQ 189
US-09-927-112-10 US-09-955-518-20 US-09-976-740-43 US-10-023-529-43 US-10-023-529-43 US-10-233-885-44 US-10-233-885-14 US-10-039-1855-1 US-10-039-1855-1 US-09-854-133-216 US-09-854-133-216 US-09-854-133-216 US-09-854-133-216 US-09-86-464-17 US-09-96-464-17 US-09-96-3285-2 US-09-963-285-2 US-09-963-285-2 US-09-963-285-2 US-09-963-285-10	ALIGNMENTS 9975253 and Compositions for Treat Human Interferon Regulatory US/09/975,253 10-12 0/239,963 13 ials Ile, Leu, Phe, or Val	Score 454; DB Pred. No. 2.1e- 63; Mismatches	EGLOWLDEARTCFRVPWKI   : :::     :    EGVAWVNKSRTRFRIPWKI	RAGWKTNFRCALRSTRRFY             WKRNFRSALNRKEGLI	PPPQGGPPGPFLAHTHAGI          PDTNGG
0.00	pplication US/09 20020164694A1 MATION: MATION: MATION: MOOSE et al. ENTION: Welhods ENTION: Using H CCE: PP196P1 ICATTON NUMBER: NG DATE: 2001-1 O ID NOS: 2 tentin Ver. 2.1 tentin Ver. 2.1 isc_feature MATION: Xaa equa	16.6%; imilarity 28.0%; ; Conservative	PRVLFGEWLLGEISSGCY 	WPPSSRGGGPPPEAETAE :	WREGPGTDQTEAEAPAAVPPPQGG 
20 21 23 23 24 24 25 25 26 27 27 29 30 30 31 31 31 31 31 31 31 31 31 31 31 31 31	RESULT 1  US-09-975-253-2  Sequence 2, Applicat Patent No. US2002016 GENERAL INFORMATION: APPLICATION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: PF1 CURRENT APPLICATION CURRENT APPLICATION CURRENT APPLICATION CURRENT PILING DATE PRIOR APPLICATION OF SOFTWARE: PRIOR PILING DATE: NUMBER OF SEQ ID NO SOFTWARE: NUMBER OF SEQ ID NO SOF	Query Match Best Local S Matches 141	Oy 10 Db 6	Qy 70 TD Db 64	Oy 130 Db 111

Qy 403 PIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHL 462 ;	RESULT 3 US-09-893-519A-14 ; Sequence 14, Application US/09893519A ; Publication No. US20030027243A1 ; GENERAL INFORMATION: ; APPLICANT: THOMPSON, Craig ; APPLICANT: BUURMAN, Ed T. ; APPLICANT: BRADLEY, John ; APPLICANT: BRADLEY, John ; APPLICANT: BRADLEY, John ; APPLICANT: BRADLEY, John ; APPLICANT: ARRES, Sandra	# APPLICANT: KOMENNITKY, Svetlana # APPLICANT: MENDILLO, Marc # APPLICANT: MCORE, Daniel # APPLICANT: MCORE, Daniel # APPLICANT: MCORE, Daniel # APPLICANT: SANDERSON, Karen # APPLICANT: SANDERSON, Karen # APPLICANT: HAQ, Tariq # APPLICANT: HOQ, Tariq # APPLICANT: APPLICANT: ON SUMIEVURGE COMPOUNDS AND METHODS OF USE # TITLE REFERENCE: 0342/10548-US2 # CURRENT APPLICATION NUMBER: US/09/893,519A # CURRENT PILING DATE: 2001-06-28 # PRIOR APPLICATION NUMBER: US 60/215,164 # PRIOR PILING DATE: 2000-08-10 # PRIOR FILING DATE: 2000-08-10 # NUMBER OF SEQ ID NOS: 146 # SOFTWARE: PatentIn version 3.1	LENGTH: 1023   TYPE: PRT   ORGANISM: Homo sapiens   FEATURE:   NAME/KRY: misc feature   OTHER INFORMATION: Corresponds to SEQ ID NO: 87   PUBLICATION INFORMATION:   DATABASE ACCESSION NUMBER: Human Genbank/CAA72189   DATABASE ENTRY DATE: 1997-06-25   RELEVANT RESIDUES: (1)(1023)	Query Match 6.1%; Score 167; DB 9; Length 1023; Best Local Similarity 24.6%; Pred. No. 0.0077; Matches 102; Conservative 22; Mismatches 131; Indels 160; Gaps 20; Qy 62 AWAVARGRWPPSSRGGGPPPEAETARAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKV 121	0y   122 YALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPL 172
	QY         368 ARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFGELVFFR 418           Db         283 AQRLGHCHTYWANSEELLPNSGHGPDGEVPKOKEGGVFDLGPFIVDLITFT 333           QY         419 ARQRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDL 478           Db         334 EGSGR-SPRYALWFCVGESWPQDQPWTKRLVWKVVPTCLRALVEMARVGGASSLENT-V 391           QY         479 DLCLSSANALYDDIECFLMEL 499           Db         1   1   1   1   1   1   1   1   1   1	RESULT 2  Sequence 374, Application US/09809391  Sequence 374, Application US/09809391  GENERAL INFORMATION:  APPLICATION  TITLE OF INVENTION: 186 Human Secreted proteins  FILE REFERENCE: PZ002P2  CURRENT APPLICATION NUMBER: US/09/809,391  CURRENT FILING DATE: 2001-03-16  Prior application data removed - consult PALM or file wrapper  NUMBER OF SEQ ID NOS: 761  SOFTWARE: PRECNIT ON NOS: 761  SEQ ID NO 374  LENGTH: 373  TYPE: PRT  ORGANISM: Homo sapiens	NAME/KEY: SITE 1 LOCATION: (175) COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE 1 LOCATION: (373) COTHER INFORMATION: Xaa equals stop translation US-09-809-31-374 Query Match  Query Match Best Local Similarity 25.2%; Pred. No. 3.7e-09; Matches 100; Conservative 59; Mismatches 165; Indels 73; Gaps 15;	QY         115 PADPHKVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPA 174           Db	QY         231         PAGELYGWAVETTPSPGPQPAALTTGBAAAPESPHQAEPYLSPSPSACTAVQEPSPGALD         290           Db         93         PEAVPKTEPLEMEVPQAPIQPPSSPELMISSLPMTDLD         132           QY         291         VTIMYKGRTVLQKV-VGHP-SCTFLYGPPDPAVRATDPQQVAFPSPAELEDQKQ         342           Db         133         IKPQYRGKEYGQTMTVSNPQGCRLEYGDLGPMPDQEELFGPVXLEQVKFPGPEHITNEKQ         192           QY         343         LRYTEELLRHVAPQLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDT         402           PD         193         KLFTSKLLDVWDRGLILEVSGHAIYAIRLCQCKVYWSGPCAPSLVAPNLIERQKKV         248

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173 PAPAGDKGDLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------APARAPRAAAAAAAATAPPSPGPAQPG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 GELYGWAVETTPSPGPPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 PR----AQRAAPLAAPPAAPPAAPPAGPRRA-----PPPAAAVAARE-SP----- 214
                                                                                                                                                                                                                                                                                                                                                                62 AWAVARGRWPPSSRGGGPPPEAETAE-----RAGWKTNFRCAL--RSTRRFVMLRDNS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 GDPADPHKVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 TPPAPPRAP-----PGGP----AAAAAPPPTPAPPP------PAPV 139
                                                                                                                                                                                                                                                                                                                                                                                                                 ------RRHGPEPERTRAELEKLIQQRAVLRVSYKGSISYRNAARVQPPRRGA 107
                                                                                                                                                                                                                                                                                       20 AAAASSSAASPHYQEWILDTI------DSLRS------RKARPDL-ERICRMVR 60
                                                                                                                                                                                                                                                 2 ALAPERAAPRVLFGEWILGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 IMYKGRIVLQKVVGHPSCIFLYGPPDPAVRAIDPQQVAFPSPAELPDQKQ 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LPPPPQP----PAPPQQQQPPPPPPQQPQ 241
                                                                                                     .5; DB 9; Length 550;
                                                                                                                                     5.5%; Score 150.5; DB 9;
23.4%; Pred. No. 0.044;
tive 20; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR PELING DATE: 2000-07-14
PRIOR PELING DATE: 2000-07-14
PRIOR PELING DATE: 2000-07-14
PRIOR PLILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1907-11-26
PRIOR PELICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1997-11-27
PRIOR PILING DATE: 1997-06-03
PRIOR PILING DATE: 1997-06-03
PRIOR FILING DATE: 1997-06-03
PRIOR FILING DATE: 1997-06-03
PRIOR FILING DATE: 1997-06-03
PRIOR FILING DATE: 1997-06-03
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Patent No. US20020129388A1
GENERAL INFORMATION:
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; LENGTH: 550
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-976-740-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 AAA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
                                                                                                                                                                   Best Local Similarity 23.4
Matches 82; Conservative
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                                                                                                                                                                                             297 PPPAAAQNGGSAGAAPAPAPAAGGPAGVSGQPGPGAAAAPAPAPAFSVATSP-----KRV 348
                                                                                 251 AAPSPPAAPAPAAPAPPPPPPPA-----PATLARPPGHPA----GPPTAAPAVP 296
                                                                                                                                        -----PAVRATDPQQV-----AFPSP---AELPDQKQLRYTEEL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Simon M.
APPLICANT: Lees, Simon M.
APPLICANT: Lees, Ann M.
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCIEROSIS
TITLE OF INVENTION NUMBER: US/09/976,740
CURRENT FILING DATE: 2000-07-14
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 76, Application US/09919497
; Sequence 76, Application US/09919497
; Patent No. US2020106662A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR PILING DATE: 2000-07-31
; PRIOR PILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 76
; SEQ ID NO 76
                                                                                                                                                                                                                                                                                    350 LRHVAPGLH-LELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTP 403
                             HQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVGHPSCTFLYGPPD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 47
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Best Local Similarity
Matches 35; Conserv
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US-09-919-497-76
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US-09-976-740-47
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Db 140 AAAA	Simila 6; Co AVARG A\  \  \  \  \  \  \  \  \  \  \  \  \  \
Db 20 AAAASSSAASPHYGEMILDTI	

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Publication No. US20
GENERAL INFORMATION:
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Publication No. US20030082645A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Greengard, Paul
APPLICANT: Greengard, Paul
APPLICANT: Kao, Hung-Teh
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-202 CIP
CURRENT APPLICATION NUMBER: US/10/1122,805
CURRENT FILING DATE: 2002-04-15
PRIOR PILLING DATE: EARLIER FILING DATE: 1998-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 171;
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                            APPLICANT: BUCCE D. Weintraub
APPLICANT: Buriusz W. Szkudlinski
APPLICANT: University of Maryland
TITLE CANT: University of Maryland
TITLE PERERENCE: UOFMD.003C1
CURRENT APPLICATION NUMBER: US/09/813,398
CURRENT PILING DATE: 2001-03-20
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/US99/05908
PRIOR APPLICATION NUMBER: PCT/US98/19772
PRIOR APPLICATION NUMBER: PCT/US98/19772
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23.6%; Pred. No. 0.06;
cive 22; Mismatches 150;
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 561
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US20020169292A1
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US-09-813-398-23
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US-10-122-805-4
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       500 AGSPLPQRL-----PSPTSAPQQPASQAAPPTQGQGRQSRPV----AGGPGAPP--- 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          545 ---AARPPASPSPORQAGPPOATROTSVSGPAPPKASGAPPGGQOROGPPOKPPGPAGPT 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                602 RQASQAGPVPRTGPPTTQQPRPSGPGPAGAPKPQLAQKP----SQDVPPPATAAAGGPP- 656
                                                                                                                                                                                                                                                                                                                                                                                                                                 133 GPGTDQTEAEAPA-AVPPPQGGPPGPFLAHTHAGLQAPGP----LPAPAGDKGDLLLQAV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445 GRQTSQQPAGPPAQQEPPPQGGPPQP-----GPGPQRQFPLQQRPPPQGQQHLSGLGPP 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 QQSCLADHLLTASWGADPVPTKAP-----GEGQEGLPLTGACAGGPGLPAGEL 235
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/906,865
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
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APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: APPLICANT: AND JAMON WETHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS OF PANCREATIC CANCER
                                                                                                                                                                                                                                                                                                        Query Match 5.4%; Score 148; DB 9; Length 690
Best Local Similarity 27.1%; Pred. No. 0.082;
Matches 73; Conservative 12; Mismatches 94; Indels
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23.4%; Pred. No. 0
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CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 159
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NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 696
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; ORGANISM: Homo sapiens
US-10-060-036-159
                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-122-805-4
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q. ;	GPGSRGFPGADGVAGPKG-PAGE	bb 592
<u>ያ</u>	241 ETTPSFUPQPAALTTGEAAAPESPHQAEPYLSESPSACTAVQEBSFGA 288  511RGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAG 560	RESULT 13
ò	289 LDVTIMYKGRTVLQKVVCHPSCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEE 348	US-10-216-705-21 ; Sequence 21, Applie
QQ	561 QDGPPGPPGPPGARGQAGVMGFPGPKGAAGE 591	; FUDITCACION NO: US; ; GENERAL INFORMATION ; APPLICANT: Merist
ò 8	349 LLRHVAPGLHLELRGPQLWARRMGKCKVYWBVGGPPGSASPS 390	; TITLE OF INVENTION TITLE OF INVENTION FILE REFERENCE: 1
		; CURRENT APPLICATION ; CURRENT FILING DATE
RESULT US-10-1 ; Seque	RESULT 12. US-10-171-36, Application US/10171311	; PRIOR APPLICATION ; PRIOR FILING DATE ; NUMBER OF SEQ ID ]
; Publi ; GENER ; APPL	Publication No. US20030087270A1 GENERAL INFORMATION APPLICANT: Schlegel, Robert	; SOFTWARE: Patentli ; SEQ ID NO 21 ; LENGTH: 1464
APPI , APPI	APPLICANT: Chen, Yan APPLICANT: Zhao, Xumei APPLICANT: Monahan, John	; TYPE: PRT ; ORGANISM: Homo si 118-10-216-705-21
APPI	APPLICANT: Kamatkar, Shubhangi	to town word
, APPI ; APPI ; APPI		Best Local Similar: Matches 80; Con
; TITI ; TITI	TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY	Qy 66 ARGRWP
, TITI , FILE	TITLE OF INVENTION: OF CERVICAL CANCER FILE REPERENCE: MRI-035	Db 414 ARGPSG
; curr	CURRENT APPLICATION NUMBER: US/10/171,311 CURRENT FILMS DATE: 2005-206-12	Qy 126 RELCWR
PRIC	OR APPLICATION NUMBER: US 60/298,159 PILING DATE: 2001-06-13	Db 440
; PRIC	DR FILING DATE: 2001-06-13	Qy 181 DLLLQA
, PRIC	PRIOR APPLICATION NUMBER: US 60/335,936 PRIOR FILING DATE: 2001-11-14	Db 489
SOFT	NOMBER OF SEQ ID NOS: 238 SOFTWARE: FastSEQ for Windows Version 4.0	Oy 241 ETTPSP
NET :	SEQ ID NO 35 LENGTH: 1464	   Db 511RGSP
, ORG	INTER PRI PORTO BADIENS	Qy 289 LDVTIM
-01-00		561 QD
Query M	Match 5.4%; Score 148; UB 9; Length 1464; Local Similarity 23.4%; Pred. No. 0.18; 6.00. Tadol 152.	Qy 349 LLRHVA
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ò	RELCWREGPGTDQTEAEAPAAVPPQGGPPGPFLAHTHAGLQA-PGPLPAPAGDKG	US-10-149-352-2 ; Sequence 2, Applic
qq		; Publication No. US ; GENERAL INFORMATION
ò	181 DLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAV 240	; APPLICANT: Beri, ; TITLE OF INVENTIO
qq		; FILE REFERENCE: 0 ; CURRENT APPLICATI
ò	241 ETTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGA 288	; CURRENT FILING DA' ; PRIOR APPLICATION · PRIOR FILING DATE
Dp	511RGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAG 560	PRIOR APPLICATION
ò	289 LDVTIMYKGRTVLQKVVGHPSCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEE 348	; NUMBER OF SEQ ID ; SOFTWARE: PatentI
QQ	561 QDGRPGPPGPPGARGQAGVMGFPGPKGAAGE 591	; SEQ ID NO 2
à	349 LLRHVAPGLHLELRGPQLMARRMGKCKVYWEVGGPPGSASPS 390	TYPE: PRT

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TION: Recombinant Collagens and Their Uses
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TION NUMBER: US/10/216,705
DATE: 2002-08-09
DN NUMBER: US 09/331,347
TE: 1999-08-17
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rity 23.4%; Pred. No. 0.18;
nservative 11; Mismatches 89; Indels 162; Gaps
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TION NUMBER: PCT/GB00/04741
ATE: 2000-12-12
TION NUMBER: GB 9929487.8
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Search completed: June 18, 2003, 12:57:02 Job time : 53 secs
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Publication No. US20030073144A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Lodges, Michael D.
APPLICANT: Persing, David H.
APPLICANT: Persing, Value T.
APPLICANT: APPLICANT: Presing, Value T.
APPLICANT: APPLICANT: Hepler, Walliam T.
APPLICANT: APPLICANT: APPLICANT: TELE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF PANCREATIC CANCER FILE REFERENCE: 210121.566
                                                                   DB 9; Length 1464;
0.18;
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                                                                 Query Match 5.4%; Score 148; DB Best Local Similarity 23.4%; Pred. No. 0.18 Matches 80; Conservative 11; Mismatches
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CURRENT FILING DATE: 2002-01-30
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963 -- AKGEPG--- FRGPPGPYGRPGYKGEIGFPGRPGRPGRNGLKGEKG---- EPGDASLG 1012 --- 1044 359 LELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFR 418 302 OKVVGHPSCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPG---LH 358 918 PGPAGPKGNLGSKGERGSPGPKGEKGEP-----GSIFSPDGGALGPA--QKG---

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unconventional myc	synapsin I - rat	synapsin Ia - rat	hypothetical prote	mullerian inhibiti	hypothetical prote	collagen alpha 1(I	collagen alpha 1(I	hypothetical prote	collagen alpha 1(X	collagen alpha 1(I	collagen 1 - Caeno	KIAA0641 protein -	eyelid - fruit fly	collagen alpha 1(X	collagen alpha 2(X
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## ALIGNMENTS

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C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 20-Jun-2000
C;Accession: JGG520
R;Hatada, S.; Kinoshita, M.; Takahashi, S.; Nishihara, R.; Sakumoto, H.; Fukui, A.; Noda
Gene 203, 183-188, 1997
                                                                                                                    interferon regulatory factor 5 - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C;Accession: G02474
R;Grossman, A.; Mittrucker, H.W.; Lantonio, L.; Mak, T.W.
Submitted to the BNBL Data Library, March 1996
A;Reference number: H0138
A;Accession: G02474
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-504 GGRO-
A;Cross-references: EMBL:U51127; NID:g1255254; PIDN:AAA96056.1; PID:g1255255
C;Genetics: Humirf5
C;Superfamily: lymphoid-specific interferon regulatory factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKIY----EVC-SNGP-----APTDSQPPEDYSFGAGEEEEEEELQRMLPSLSLTD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275
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GRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDLCLSSANSLYDDIECFLMELE 500
                    HKVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPG------PFLAHTH 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---QVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGGPP 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PGNPAGFRELLSEVLE----PGPLPASL-----PPAGEQLLPDLLISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 SACTAVQEPSPGALDVTIMYKGRTVLQKVVGHP-SCTFLYGPPDPAVRATDPQ----
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                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 482.5; DB 2; Length 504; Pred. No. 3.8e-22; 60; Mismatches 194; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 30.0%;
Matches 155; Conservative 6
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A, Contents: Embryo
A, Accession: JG5210
A, Moceule type: mRNA
A, Residues: 1-459 - FHAT>
A, Residues: 1-459 - FHAT>
A, Cross-references: DDBJ: D86492; NID: 92780409; PIDN: BAA24349.1; PID: 92780410
C, Comment: This protein plays a role in the transcriptional regulation of specific genes
A, Gene: xIRP-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lymphoid-specific interferon regulatory factor - mouse
NyAlternate names: Pip PU.1 interaction partner
C,Species Mus musculus (house mouse)
C;Species Mus musculus (house mouse)
C;Species: Mas musculus (house mouse)
C;Accession: S57837; S57838; I49359
C;Accession: S57837; S57838; I49359
C;Accession: S57837; S57838; I49359
R;Attle: Molecular cloning of LSIRF, a lymphoid-specific member of the interferon regulat A;Teference number: S57836; MUID:95334364; PMID:7541907
A;Accession: S57837
A;Accession: S57837
A;Accession: S57837
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-450 <AMAI>
A;Residues: 1-450 <AMAI>
A;Cross-references: EMBL:U20949; NID:9972947; PIDN:AAA75316.1; PID:9972948
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
A;Note: only a part of the coding sequence is given
R;Matsuyama, T.; Grossman, A.; Mittruecker, H.; Sideroveki, D.; Kawakami, T.; Kimura, T., submitted to the EMBL Data Library, June 1994.
A;Title: An interferon regulatory factor-related gene (xIRF-6) is expressed in the poste A;Reference number: JC6520; MUID:98086218; PMID:9426249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 GELYGWAVETTPSPGPQPAAL--TTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALD 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 VTIMYKGRTVLQKV-VGHP-SCTFLYGPPDPAVRATD-----PQQVAFPSPAELPDQKQ 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 IRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHL 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAMHPR----RVRLKPWLVAQVDSGMYPGLIWLNREAKRFQIPWKHATRHSPRQEEENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGD-PADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 DDDFEADELNQS------QNHVPISEPFNCLNINDSPIGSSSTGSCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MALAPERAAPRVLFGEWILGEISSGCYEGLOWLDEARTCFRVPWKHFAR-KDLSEADARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 16.1%; Score 440; DB 2; Length 459;
Best Local Similarity 27.1%; Pred. No. 1.3e-19;
Matches 140; Conservative 74; Mismatches 197; Indels 106; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : | : | : | EMFTGDSTRSFDSGSIRLOISIPD-IKDNIVSHLKHL 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGTQREGVSSLDSSDLDLCLSSANSLYDDIECFLMEL 499
                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: lymphoid-specific interferon regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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19;

Gaps

Indels 159; Length 424;

74 67 203

312

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291 ---VTIMYKGRTVLQKV------VGHPSCTFLYGPPDPAVRATDPQQVAFPSPAEL 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNCDTPIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWL 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 PGTDQTEAEAPAAVPPPQGGPPGFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQSCLA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DHILTASWGADPVPTKAPGEGQ-EGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQPAA 252
                                                                                                                                                                                                                                                                               RGGGPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                      113 --VPEEEQKCKLGV-----CMS 131
                                                                                                                                                                                                            253 LTTGEAAAPESPHQAEPYLSPSPSACTA-----VQEPSPG-----ALD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------PEACRSQILPDWWVQQPSAGLPLVTGYAAYDTHHSAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E------VPEMECGRSEIBELIKE-----PSVDEYMGMTKRSPSP----
                                                                                                                                                                               EWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 OMVISFYYGGKLVGQATTTCLEGCRLSLSQPGLPKLYGPD----GLEP--VCFPTADTI
C,Superfamily: lymphoid-specific interferon regulatory factor
C,Keywords: DNA binding; transcription regulation
                                                                          Query Match 12.2%; Score 333.5; DB 2; Best Local Similarity 24.3%; Pred. No. 3.4e-13; Matches 121; Conservative 65; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRVHLEGTQRE-GVSSL 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AROLVEEAGKSCGAGSL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: HeLa cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A45017
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 29-Sep-1999
C;Accession: A35661
R;Driggers, P.H.; Ennist, D.L.; Gleason, S.L.; Mak, W.H.; Marks, M.S.; Levi, B.Z.; Flans Proc. Natl. Acad. Sci. US.A. 87, 3747, 1990
A;Title: An interferon gamma-regulated protein that binds the interferon-inducible enhant A;Reference number: A35861; MUID:90251633; PMID:2111015
                                                                                                                                                    A, Cross-references: EMBL:U11692; NID:g790199; PIDN:AAA75309.1; PID:g790200
KE Bisenbels, C.F., Singh, H.; Storb, U.
Genes Dev. 9, 1377-1387, 1995
A;Title: Pip, a novel IRF family member, is a lymphoid-specific, PU.1-dependent transcri
A, Reference number: 149359; MUID:95317607; PMID:7797077
A, Accession: 149359
A, Status: translated from GB/EMBL/DDBJ
  A; Description: Molecular cloning of LSIRF, a lymphoid-specific member of the interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 CLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAG----GPGLP----AGELYGWAVE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTPSPG-PQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 ESQAPGIPIEPSIRSAEALA-----LSDC-----RLHICLYYRDILV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 LQKVVGHP-SCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 KELTTTSPEGCRISHG---HTYDVSNLDQVLFPYP---DDNGQRKNIEKLLSHLERGLVL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 ELRGPQLWARRMGKCKVYWEVGGPPGSAS--PSTPACLLPRNCDTPIFDFRVFFQELVEF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 PGTDQTEAEAPAAVPPPQGGPPGP---FLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-450 <RES>
A;Cross-references: EMBL:U34307; NID:g976446; PIDN:AAA75283.1; PID:g976447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 QWLIDQIDSGKYPGLVWENEEKSVFRIPWKHAGKQDYNREEDAALFKAWALFKGKF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 EWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.8%; Score 376; DB 2; Length 450; llarity 28.1%; Pred. No. 9.5e-16; Conservative 66; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 72/3; 135/1; 164/3; 213/1; 249/1; 367/1; 404/3
C;Superfamily: lymphoid-specific interferon regulatory factor
C;Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCR 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reference number: $57838
Accession: $57838
                                                                                                     A; Molecule type: mRNA
A; Residues: 1-450 <MAT2>
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-424 <DRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                               A;Status: preliminary
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A35861
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R;Veals, S. A.; Schindler, C.; Leonard, D.; Fu, X.Y.; Aebersold, R.; Darnell Jr., J.E.; Le Mol. Cell. Biol. 12, 3315-3324, 1992
A;Title: Subunit of an alpha-interferon-responsive transcription factor is related to int A;Reference number: A45017; MUID:92334329; PMID:1630447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
transcription factor ISGF3 gamma chain - human
N;Alternate names: alpha-interferon-responsive transcription factor
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 WLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSE-ADARIFKAWAVARGRWPPSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-393 <VEA>
A;Cross-references: GB:M87503; NID:g184652; PIDN:AAA58687.1; PID:g184653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Note: sequence extracted from NCBI backbone (NCBIP:108663)
A, Note: part of this sequence was confirmed by protein sequencing
C; Superfamily: lymphoid-specific interferon regulatory factor
C; Keywords: DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.0%; Score 328.5; DB 2; 25.7%; Pred. No. 6.2e-13; tive 69; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                      Status: nucleic acid sequence not shown
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r 3 gamma (ISGF3 gamma/p48) c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    hi, T.; Kitagawa, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s 105; Gaps 14;
               :| ::| : | :|
IIPSERQRQVTRKL 270
                                                  LLPRNCDTPIFDFR 408
                                                                                                        PWLCRVHLEGTQRE 468
                                                                                                                           :::: | ...--QLYVRQLAEE 379
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VYRILPAGTLPNOP 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYGWAVETTPSPGP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 QPAALITGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVGHP 308
AELPDQKQLRYTEEL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --ĠGNĠS----- 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AWAVARGRWPPSSR 75
|||:::
AWALFKEK----- 68
                                                                                                                                                                                                                                                                                                                                                                                                                         1; PID:91263310
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Oy 18 LLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVARGRWPPSSRGG 77 14    1    1    1    1    1    1	Qy         227 GPGLPA-GELYGWAVETTPSPGPQPAALTTGEAAAPESSPHQAEPYL 271           Db         363 APGTAGPAPGTASYAPGTAPAPGTAPAPGTAGPARDTSYAPGTAPAPGT 422           Qy         272 SPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVGHPSCTFLYGPPDPAVRAT 324           Db         423 APAPGSTPAPGTVPAPGTAPAPGPQPADGRRPVTGPASGTGPGAAT 468           Qy         325 DPQQVAFPSPA 335           Db         469 PPEAAAAASAGSAPSPA 485           RESULT 11           152998           interferon regulatory factor 1 - human	C;Species: Homo sapiens (man) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999 C;Accession: 152998 R;Cha, Y.; Sims, S.H.; Romine, M.F.; Kaufmann, M.; Deisseroth, A.B. DNA Cell Biol. 11, 605-611, 1992 A;Title: Human interferon regulatory factor 1: intron/exon organization. A;Reference number: 152998; MUID:93000481; PMID:1382447 A;Accession: 152998 A;Actus; preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-325 <res> A;Cross-references: GB:L05072; NID:g184648; PIDN:AAA36043.1; PID:g184649 C;Genetics: A;Gene: GDB:RRF1 A;Cross-references: GBE:127269; OMIM:147575 A;Map position: 5G31.1-5G31.1 A;Introns: 29/3; 63/1: 122/1; 138/3; 182/1; 223/1; 239/3; 285/1</res>	Query Match
	RESULT 9 S57836 Ilymphoid-specific interferon regulator factor - mouse (fragments) C;5pecies Mus musculus (house mouse) C;0ate: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999 C;Accession: S57836 R;Matsuyama, T.; Grossman, A.; Mittuuecker, H.W.; Siderovski, D.P.; Kiefer, F.; Kawakami, Nucleic Acids Res. 23, 2127-2136, 1995 A;Title: Molecular cloning of LSIRF, a lymphoid-specific member of the interferon regula A;Reference number: S57836, MUID:95334364; PMID:7541907 A;Ctatus: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-203 cMAT> A;Cross-references: EMBL:U11692 C;Superfamily: lymphoid-specific interferon regulatory factor	Query Match         8.2%;         Score 224;         DB 2;         Length 203;           Best Local Similarity         34.8%;         Pred. No. 6.7e-07;         Animal Similarity         34.8%;         Pred. No. 6.7e-07;         Animal Similarity         Animal Similarity <t< td=""><td>RESULT 10 TSOS68 Probable multi-domain regulatory protein [imported] - Streptomyces coelicolor C;Decies: Streptomyces coelicolor C;Dete: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000 C;Accession: TSOS68 R;Redenbach, M.;Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw Mol. Microbiol. 21, 77-96, 1996 A;Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb SACCESSION: TSOS68 A;Reference number: Z2OSS6; MUID:97000351; PMID:8843436 A;Accession: TSOS68 A;Accession: TSOS68 A;Accession: TSOS68 A;Residues: L1334 &lt;-RED&gt; A;Residues: 1-1334 &lt;-RED&gt; A;Residues: 1-1334 &lt;-RED&gt; A;Residues: L1334 &lt;-RED&gt; A;Residues: SCC75A.05c  Query Match Best Local Similarity 28:1%; Pred. No. 0.0015; Matches 106; Conservative 25; Mismatches 150; Indels 96; Gaps 22;</td></t<>	RESULT 10 TSOS68 Probable multi-domain regulatory protein [imported] - Streptomyces coelicolor C;Decies: Streptomyces coelicolor C;Dete: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000 C;Accession: TSOS68 R;Redenbach, M.;Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw Mol. Microbiol. 21, 77-96, 1996 A;Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb SACCESSION: TSOS68 A;Reference number: Z2OSS6; MUID:97000351; PMID:8843436 A;Accession: TSOS68 A;Accession: TSOS68 A;Accession: TSOS68 A;Residues: L1334 <-RED> A;Residues: 1-1334 <-RED> A;Residues: 1-1334 <-RED> A;Residues: L1334 <-RED> A;Residues: SCC75A.05c  Query Match Best Local Similarity 28:1%; Pred. No. 0.0015; Matches 106; Conservative 25; Mismatches 150; Indels 96; Gaps 22;

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A; Molecule type: mRNA
A; Mesdidues: 1-57, RV, 59-349 <ITO>
A; Mesdidues: 1-57, RV, 59-349 <ITO>
A; Cross-references: EMBL:X15949; NID:933966; PIDN:CAA34073.1; PID:933967
R; Harada, H.; Fujita, T.; Miyamoto, M.; Kimura, Y.; Maruyama, M.; Furia, A.; Miyata, T.;
R; Harada, H.; Fujita, T.; Miyamoto, M.; Kimura, Y.; Maruyama, M.; Furia, A.; Miyata, T.;
A; Title: Structurally similar but functionally distinct factors, IRF-1 and IRF-2, bind to
A; Reference number: A32828; MUID:89354547; PMID:2475256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Miyamoto, M.; Fujita, T.; Kimura, Y.; Maruyama, M.; Harada, H.; Sudo, Y.; Miyata, T.; (2011 54, 903-913, 1988
A;Title: Regulated expression of a gene encoding a nuclear factor, IRF-1, that specifica. A;Reference number: A90903; MUID:88311092; PMID:3409321
A;Accession: B31595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-68,11,70-96,7R',98-130,'ER',133-152,'GF',155-163,'A',165-188,'D',190-210,'
A;T',310-313,'PAPV',318-319,'TP',322-349 <HAR>
A;Cross-references: GB:003168; NID:9198455; PIDN:AAA39333.1; PID:9293676
A;Experimental source: clones 2 and 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujita, T.; Kimura, Y.; Maruyama, M.; Harada, H.; Sudo, Y.; Miyata, T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interferon regulatory factor 1 - human
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 RVLFGEWILGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 WLLGEISSGCYEGLQWLDEARTCFRVPWKHFARK--DLSEADARIFKAWAVARGRWPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Gaps
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                           A;Cross-references: GB:L24442
K*Itch, S.; Harada, H.; Fujita, T.; Mimura, T.; Taniguchi,
Nucleic Acids Res. 17, 8372, 1989
A;Title: Sequence of a CDNA coding for human IRF-2.
A;Reference number: S06894; MUID:90045964; PMID:2813069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 HQP----GVDKPDPKT-----WKANFRCAMNSLPDIEEVKDKS
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Ribesidues: 17-325 cMR>
Ribesidues: 17-325 cMR>
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1 Similarity 23.4%; Pred. No. 0.0036;
67; Conservative 33; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
6.1%; Score 167; DB 2;
Best Local Similarity 35.0%; Pred. No. 0.0034;
Matches 36; Conservative 18; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GDB:127270; OMIM:147576
A;Map position: 4q35.1-4q35.1
C;Keywords: DNA binding; transcription regulation
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C;Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: B31595; S04075
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Matches 67; Conserv
Residues: 1-349 <CHA>
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NiAlternate names: transcription repressor IRF2
C;Species Homo sapiens (man)
C;Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 05-Nov-1999
C;Accession: A53340; 806894; A32828
C;Accession: A53340; 806894; A32828
A;Title: Human interferon regulatory factor 2 gene. Intron-exon organization and functic A;Accession: A53340.
A;Reference number: A53340; MUID:94148994; PMID:8106512
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-174,'X',176-233,'X',235-344,'X',346-408,'X',410-499,'X',501-876,'X',878-11
A;Cross-references: GB:M60172
C;Superfamily: unassigned collagens
C;Keywords: cornea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432 QQGPRGEKGSAVEVVIETIKTEVSSLASQMLSDLQGRAGPPGPPGPPGESVQGLP---GP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVGHPSCTFLYGPPDPAVRATDP---- 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               534 PGPRGFTG--EPGEPGLPGFSSHGGTVTMQGPPGPP-----GPPGPKGDAGVPGAPGIP 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GEPGA 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --APAGDKG---DLLLQAV--QQSCLADHLLTASWG--ADPVPTKAPGEGQEGLPLTGAC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGPGLPAGELYGWAVETTPS--PGPQPAALTTGE--AAAPESP------HQAEPYLS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGPPGLPG-----PSGPPGRPGSSVSTSETFVSGPPGPPGPKGDQGE---- 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 -----QQV----AFPSPAELPDQKQLRYTEELL----RHVAPGLHLELRGP 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388 PGKVIS------AEGSSTIALPGPP-GPPGPIGPTGPPGVGPAGLPG 431
                                                                                                                         C;Species: Gallus Gallus (chicken)
C;Species: Gallus Gallus (chicken)
C;Date: 14-Feb-1992 #sequence_revision 15-Aug-1997 #text_change 20-Sep-1999
C;Accession: S16501; Associate T.F.; Gordon, M.K.
R;Marchant, J.K.; Lineenmayer, T.F.; Gordon, M.K.
Proc: Natl. Acad. Sci. U.S.A. 88, 1560-1564, 1991
A;Title: CDNA analysis predicts a cornea-specific collagen.
A;Reference number: A38587; MUID:91142213; PMID:1705041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 ARGRWPPSSRGG-----GPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPAD
                                                                                                                                                                                                                                                                                                                                                                   A;Accession: S16501
A;Molecule type: mRNA
A;Residuss: 1-1146 <MAR>
A;Cross-references: EMBL:M60172; NID:g211609; PIDN:AAA48703.1; PID:g211610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 6.4%; Score 176; DB 2; Length 1146; Local Similarity 23.8%; Pred. No. 0.0033; les 109; Conservative 31; Mismatches 132; Indels 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 ARGPPGPSGDTGEPGLTGPQGPPGLPGNPGRPGAK----
                                                                                                 chicken
                                                                                                 collagen, cornea-specific -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A38587
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Best Local Si
Matches 109;
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C;Accession: A31595
R;Miyamoto, M.; Fujita, T.; Kimura, Y.; Maruyama, M.; Harada, H.; Sudo, Y.; Miyata, T.;
Cell 54, 903-913, 1988
A;Title: Regulated expression of a gene encoding a nuclear factor, IRF-1, that specifica A;Reference number: A90903; MUID:88311092; PMID:3409321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-329 <MIY>
A;Cross-references: GB:M21065; NID:g198458; PIDN:AAA39334.1; PID:g293677; GB:J03160; GB:
C;Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
66 KAGEKEPDPKT-----WKANFRCAMNSLPDIEEVKDGSRNKGSSA--VRVYRMLPPLTKN 118
                                                                               130 -WREGPGTDQTEAEAPAAVPPPQGGPPGPF-----LAHTHAGLQAPGPLPAPAGDKG 180
                                                                                                                                                                                                                                  169 -----YMQDLEVEQALT-------PALSPCAVSSTLPDWHIPVEVV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:||
113 PPLTRNQRKERKSKSKDTKSKTKRKLCGDVSPDTFSDGLSSSTLPDDHSSYTTQGYLGQ 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 GDKGDLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELY 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 RWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRD---NSGDPADPHKVYAL- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----DQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQ-------APGPLPAPA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 RVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARK--DLSEADARIFKAWAVARG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                        interferon regulatory factor 1 - mouse
C,Species: Mus musculus (house mouse)
C,Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.1%; Score 166; DB 2; Length 329;
Best Local Similarity 21.6%; Pred. No. 0.0036;
Matches 65; Conservative 40; Mismatches 88; Indels 108; Gaps
                                                                                                                                                                                181 DLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLP-
                                                                                                                              119 ORKERKSKSSRDAKSKAKRKSCGDSSPDTFSDGLSSSTLPDDHSSYTVPG-
                                                                                                                                                                                                                                                                                                                       203 PDSTSDLYNFQV----SPMPSISEATTDEDEEGKLPEDIMKLLEQS 244
                                                                                                                                                                                                                                                                                  232 ---AGELYGWAVETTPSPGPOPAALTTGEAAAPESPHQAEPYLSPS 274
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GenCore (c) 1993
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OM protein - protein search, using sw model

May Run on:

US-09-647-965-9 2731 Title: Perfect score:

1 MALAPERAAPRVLFGEWLLG......SANSLYDDIECFLMELEQPA

503

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_16Dec04:\* 1: geneserm1000-Database :

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2004s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMARTES

	Description	Aay15103 Modified	Adj75462 Marker ge	Marker	Human F	Ade58669 Human Pro	Aae09329 Human int	Adj75465 Marker ge	Marker	Ad183070 Human PRO	Adn04327 Antipsori	Adp24098 PRO polyp		Adj75463 Marker ge	Human d	Abm83031 Human dia	Abm83029 Human dia	Abm83032 Human dia	Adg77002 Human nuc	Abm83033 Human dia	Abm83034 Human dia	Aay15104 Chimeric	Ade58663 Rat Prote	Rat	Adj76202 Marker ge	Marker
SUMMAKIES	ID	AAY15103	ADJ75462	ADJ75410	ADE58665	ADE58669	AAE09329	ADJ75465	ADJ75413	ADL83070	ADN04327	ADP24098	ADJ75411	ADJ75463	ABM83030	ABM83031	ABM83029	ABM83032	ADG77002	ABM83033	ABM83034	AAY15104	ADE58663	ADE58667	ADJ76202	ADJ76237
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Adr99903 Immune Re	Adr99902 Immune Re	Adj75464 Marker ge	Adj75412 Marker ge	Adr14355 Human NF-	Abm83016 Human dia	Abm83017 Human dia	Abm83019 Human dia	Abm83020 Human dia	Add01173 Human nuc	Abm83015 Human dia	Abm83018 Human dia	Adg77016 Human nuc	Abm84398 Human dia	Aam78986 Human pro	Abm82144 Tumour-as	Adq39628 Human myo	Adq39630 Human myo	Aay87783 Human IRF	Abg76085 Human int
ADR99903	ADR99902	ADJ75464	ADJ75412	ADR14355	ABM83016	ABM83017	ABM83019	ABM83020	ADD01173	ABM83015	ABM83018	ADG77016	ABM84398	AAM78986	ABM82144	ADQ39628	ADQ39630	AAY87783	ABG76085
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247	186	164	164	164	496	476	476	476	488	491	491	455	455	427	427	427	427	427	427
46.3	30.9	30.5	30.5	30.5	18.2	17.9	17.9	17.9	17.7	17.7	17.7	17.2	17.2	16.8	16.8	16.8	16.8	16.6	16.6
1264.5	843	832	832	832	497.5	487.5	487.5	487.5	484.5	484	484	469	469	458	458	458	458	454	454
26	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

Interferon regulatory factor; IRF-7; transactivation domain; serine; threonine; carboxy terminus; aspartic acid; mutant; phosphorylation; sost-translational modification; sendai virus; cancer treatment; herpes; activator; promoter; ISRE regulatory element; stimulation; influenza; DNA binding; transcriptional activity; viral infection; HIV infection; activate; homology; cytokine gene; target cell. Modified Interferon Regulatory Factor-7 protein (IRF-7). AAY15103 standard; protein; 503 AA (first entry) 25-JAN-2000 AAY15103; RESULT 1 AAY15103 

sapiens. Synthetic. Ношо

/note= "Wild type Ser replaced with Asp" /note= "Wild type Ser replaced with Asp" Location/Qualifiers Misc-difference 477 Misc-difference 479 WO9951737-A1

14-OCT-1999.

99WO-CA000314. 07-APR-1999; 98CA-02234588. 07-APR-1998; (DAVI-) DAVIS-JEWISH GEN HOSPITAL MORTIMER B.

Hiscott J, Lin R;

WPI; 1999-620201/53. N-PSDB; AAX90993 Carboxy-terminus modified highly active forms of interferon regulatory factor proteins used for the treatment of viral infections.

Claim 14; Fig 12; 93pp; English.

The present protein sequence is the interferon regulatory factor-7 (IRF-  $^{7}$ ) 2D protein, that is modified in the transactivation domain. The serine

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and threonine residues in the carboxy terminus are modified post-
translationally, by phosphorylation, following sendai virus infection. The modified IRF-7, substituted with aspartic acid, functions as a
activator of promoters containing ISRE regulatory elements and
stimulation of DNA binding and transcriptional activity. IRF-7 protein
shows highest homology to IRF-3. The modified IRF proteins are used for
the treatment of viral infections like, influenza, herpes or HIV
infection. They may also be used to activate a cytokine gene, in cancer
treatment or to modify a target cell of an organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLBPWLCRVHLBGTQREGVSSLDSSDLDL
                                                                                                                                                                                                                                                                                           MALAPERAAPRVLFGEWILGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIF
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                                                                                                                                                                                                                        Similarity
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DLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAV 240 ETTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTV 300 VYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKG 61 KAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHK KAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHK 1 MALAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIF DLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAV 99.6%; Score 2719; DB 8; 99.6%; Pred. No. 9.5e-196; iive 0; Mismatches 2; Matches 501; Conservative Local Similarity 61 121 181 181 241 Query Match qq 셤 ò 유 ò ò 염 δ 8 bronchial asthma; chronic obstructive pulmonary disease; respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic; Marker gene related amino acid sequence SEQ ID NO:714. Ź ADJ75462 standard; protein; 503

(first entry)

20-MAY-2004

ADJ75462;

RESULT

gene therapy; marker

EP1394274-A2

Homo

3-MAR-2004.

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Length 503;

9 9 120 120 180 180 240

ETTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTV 300

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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises or chronic obstructive pulmonary disease. The method comprises or chronic obstructive pulmonary disease. The marker gene in a biological sample from a subject, comparing the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (31) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13, Also described: (l) a group of genes (32) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (l) a reagent (l) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma or chronic obstructive pulmonary disease, (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antiense nucleic acid corresponding to a portion of the marker gene or an antiense nucleic acid corresponding to a portion of the marker gene, and fol an DNA chip for testing for expression of the gene through an RNAi effect or an antibody recognising a probe has been immobilised to assay a marker gene. (1) has respiratory and antiasthmatic activities, and can be used in gene therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present is useful for testing for or screening for a therapeutic agent in the exemplification of the present invention.
                                                                                                                                                                                                                                                                         Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a
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                                                                                                                                                                              Nagai
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                                              06-AUG-2002; 2002JP-00229312
20-MAR-2003; 2003JP-00077212
04-AUG-2003; 2003EP-00254857
                                                                                                                          (GENO-) GENOX RES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13, or (b) a group of genes (S2) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13, or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are trimulated with interleukin-13. Also described: (1) a reagent (1) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma or chronic
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                                                                                                                                                                                                                                                                                                                                                                                                          sthma; chronic obstructive pulmonary disease; epithelial cell; interleukin-13; respiratory; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a healthy subject.
               LRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRAR
                                                                                                                                               ORRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSSLSL
                                                                      LRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTP1FDFRVFFQELVEFRAR
                                                                                                                              ORRGSPRYT1YLGFGODLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Izuhara K;
                                                                                                                                                                                                                                                                                                                                                                              Marker gene related amino acid sequence SEQ ID NO:662.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 11; SEQ ID NO 662; 241pp; English.
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20-MAR-2003; 2003JP-00077212.
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                                                                                                                                                                                                                                                                                                                                                                                                                             respiratory epithelia
gene therapy; marker.
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obstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (1) has respiratory and antiaethmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polyneptides or their antibodies. The polynucleotide or the compound that method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that medulates its activity is useful for preparing a medicament for treating pain and spared nerve injury (SNI) in an animal (e.g. gene herapy). The sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed the sequence as obtained in electronic form directly from WIPO at the print of the interval of the printed the contract of the printed the contract of the contract 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDEG 180
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                                                                                                                                                                                                                                                                                                                                                                 New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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Pred. No. 1.9e-195;
1; Mismatches 2;
                                                                                                                                                                                                                                                              Costigan M;
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                                                                                                                                                                                                                                                              Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page; 1017pp; English.
                                                                                                     14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                               14-AUG-2002; 2002WO-US025765
                                                                                                                                                                                          (GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
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Best Local Similarity
Matches 500; Conserva
                                                                                                                                                                                                                                                            Woolf C, D'urso D,
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                      27-FEB-2003
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also comprising the novel polynucleotide, a host collomptising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the contribition and compound that regulates the activity of one or more of the contribition.
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                                                                                                                                                                                                                                    New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic construction injury (CCI) and spared nerve injury (SNII)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                               New genes encoding intracellular regulatory molecules, useful for regulating cell division and proliferation (e.g. tumor cells), particularly for treating cancer, infections, wounds, or developmental metabolic abnormalities.
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98.7%; Score 2695; DB 4;
Best Local Similarity 99.0%; Pred. No. 6.1e-194;
Matches 498; Conservative 0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention
                                                                                                                                                                                                                                                          bronchial asthma; chronic obstructive pulmonary disease;
respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Testing for bronchial asthma or chronic obstructive pulmonary disease by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a
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                                                                                                                                                                                                              Marker gene related amino acid sequence SEQ ID NO:717.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 11; SEQ ID NO 717; 241pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kubo H,
                                                                    standard; protein; 516 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamaya M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-AUG-2003; 2003EP-00254857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-2002; 2002JP-00229312.
20-MAR-2003; 2003JP-00077212.
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                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                            gene therapy; marker
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    healthy subject
                                                                                                                                                                                                                                                                                                                                                                                                    EP1394274-A2
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                               20-MAY-2004
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                                                                                                                 ADJ75465;
                                                                    ADJ75465
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379
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                                                                                                                                                                                                                                                                                                                                                 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 GPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366
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                                                                                                                                                                                                                                                                                                                                                                                                       200 VQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDLCLSSAN 486
  99
                                                     79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bronchial asthma; chronic obstructive pulmonary disease;
respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 HPSCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSSLSLCLSSAN
                                RGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSR
                                                                                                                                                  RGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSR
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7 RAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVA
                                                                                                                                                                                                                                   ELCWREGPGTDQTEARAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQA
                                                                                                                                                                                                                                                                                                                                                 VOOSCLADHLLTASWGADPVPTKAPGEGOEGLPLTGACAGGPGLPAGELYGWAVETTPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 GPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307 HPSCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WARRMCKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marker gene related amino acid sequence SEQ ID NO:665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ75413 standard; protein; 516 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLYDDIECFLMELEQPA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLYDDIECFLMELEQPA 503
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20-MAR-2003; 2003JP-00077212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugita Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-193155/19.
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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level determined with the expression level as pronchial sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels descrease when respiratory epithelial cells are trimulated with interleukin-13. Also described: (1) a reagent (1) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma in a mouse; (5) a mathod for producing an animal model for bronchial asthma in a mouse; (5) a pherior in a mulmonary disease; (4) an inducer that induces bronchial asthma in chronic obstructive pulmonary disease; (5) a pherior in a mouse of thouse the producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (5) a pherior in a mouse; (5) a pherior in a mouse of chronic obstructive pulmonary disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       obstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antiseanse nucleic acid corresponding to, a portion of the marker gene, a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.
                                                                 Example 11; SEQ ID NO 665; 241pp; English.
subject
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Sequence 516 AA;

140 ELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDGGDLLLQA 199 246 380 WARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFPRELVEFRARQRRGSP 439 RGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSR 126 80 RGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSR 139 186 200 VQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSP 259 306 260 GPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVG 319 HPSCTFLYGPPDPAVRATDPQQVAFPSPAELPDQXQLRYTEELLRHVAPGLHLELRGPQL 366 WARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRGSP 426 RYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDLCLSSAN 486 99 20 RAAPRVLFGEWLLGEISSGCYEGLOWLDBARTCFRVPWKHFARKDLSEADARIFKAWAVA 79 VQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSP 247 GPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVG RAAPRVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVA **ELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQA** Gaps ő Length 516; 2; Indels Score 2682; DB 8; Pred. No. 5.9e-193; 2; Mismatches 2; 98.2%; 99.2%; Matches 493; Conservative Query Match Best Local Similarity 307 320 367 427 67 127 187 g g ઠે 셤 δ g δ 유 ò 엄 ò 유 ò 8

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126 139

487 SLYDDIECFLMELEQPA 503

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The present invention relates to PRO proteins and their coding sequences. The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. x-linked infantile hypogammaglobulinemia, polysaccharide antigen unresponsiveness, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency of IgG subclasses, immunodeficiency with hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's lymphoma, intermediate lymphoma, follicular lymphoma, type II hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic ansemia, mysathenia gravis, hypoatenocorticism, glomerulonephritis, or anklylosing spondylitis. The PRO proteins are also useful for preparing a medicament for treating a condition that is responsive to the PRO mon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 RAAPRVLFGEWILGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVA 79
                                                                                                                                                                                                                                                              Immunosuppressive, Cytostatic; Antiarthritic; Antirheumatic; Antianemic; Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory; Gene Therapy; PRO; B cell related disorder; cancer; immune-mediated inflammatory disease; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probbes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in curn are useful in the development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 RGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and screening of therapeutically useful reagents.
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Pred. No. 5.9e-193;
2; Mismatches 2;
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                                                                                                                 ADL83070 standard; protein; 516 AA
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Human PRO83673, SEQ ID 272
                                                                                                                                                                                       (first entry)
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nes 493; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADL83069
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                                                                                                                                                                                                                                                                                                                                                                                                WO2004024097-A2
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wu TD;
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ADL83070
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260 GPQPAALITGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVIIMYKGRIVLQKVVG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                                                                                                                                             20 RAAPRVLFGEWLLGEISSGGYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVA
                                                                                                                                                         80 RGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSR
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                                                                                                                                                                                                           ELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDLCLSSAN
                                                                    RAAPRVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVA
 Length 516;
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams PM,
Score 2682; DB 8;
Pred. No. 5.9e-193;
                                  2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥.
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Query Match
Best Local Similarity 99.2%;
Matches 493; Conservative
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N-PSDB; ADP24097.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WI.
                   GPQPAALITIGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVIIMYKGRTVLQKVVG
                                                                                                                                                                                                                             WARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFRELVEFRARQRRGSP
ELCWREGPGTDQTEAEAPAAVPPQGGPPGPFIAHTHAGLQAPGPLPAPAGDKGDLLLQA
                                                                                        VQQSCLADHLLTASWGADPVPTKAPGEGGEGLPLTGACAGGPGLPAGELYGWAVETTPSP
                                                                                                                                       GPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVG
                                                                                                                                                                                                                                                                               WARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRGSP
                                                                                                                                                                                                           HPSCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQL
                                                                      VQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSP
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pharmaceutical composition for diagnosing or treating psoriasis in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antipsoriatic; gene therapy; psoriasis; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN04327 standard; protein; 516
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XXX ANT 10
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XXX BO 08-A

499

M.

Wood

486

New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system

Claim 7; SEQ ID NO 1276; 2940pp; English

The invention relates to a novel isolated nucleic acid and the PRO polypoptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, osceopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, antiasthmatic, antidiabetic, dermatological, antipsoriatic, antiallergic, antiasthmatic, nepatotropic, and respiratory activity. A polymelectide of the invention may have a use in gene therapy. The PRO polypeptide, contagonist, or antibody that specifically binds to the agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, invenile chronic arthritis, a spondyloarthropathy, systemic solerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, systemic thrombocycopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, dullain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, a heptobiliary chilarinic disease, infectious or autoimmune chronic active hepticials. biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, ecsinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence represents a PRO protein of the invention

Sequence 516 AA;

Gaps ö 98.2%; Score 2682; DB 8; Length 516; 99.2%; Pred. No. 5.9e-193; ive 2; Mismatches 2; Indels Matches 493; Conservative Best Local Similarity Query Match

380 WARRMCKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFRELVEFRARQRRGSP 439 440 RYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSSLSLCLSSAN 499 RGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSR 126 80 RGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALLSF 139 ELCWREGPGTDQTEAEAPAAVPPPQGGPPGFFLAHTHAGLQAPGPLPAPAGDKGDLLLQA 186 140 ELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDEGDLLLQA 199 246 200 VQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSP 259 GPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVG 306 HPSCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQL 366 WARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRGSP 426 427 RYTIYLGFGODLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDLCLSSAN 486 7 RAAPRVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVA 66 20 RAAPRVLFGEWILGEISSGCYEGLOWIDEARTCFRVPWKHFARKDLSEADARIFKAWAVA 79 VQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSP 260 127 367 67 187 247 307 g ò g ò g ò 셤 ò 요 ઠે a ઠે 원 `∂` 셤 ઠ

500 SLYDDIECFLMELEQPA 516 487 ઠે a

ADJ75411 standard; protein; 474 AA

ADJ75411;

(first entry) 20-MAY-2004

Marker gene related amino acid sequence SEQ ID NO:663.

bronchial asthma; chronic obstructive pulmonary disease; respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic; gene therapy; marker

Homo sapiens

03-MAR-2004.

04-AUG-2003; 2003EP-00254857.

06-AUG-2002; 2002JP-00229312. 20-MAR-2003; 2003JP-00077212.

(GENO-) GENOX RES INC.

Kubo H, Nagai H, Yamaya M, Ohtani N, Sugita Y,

WPI; 2004-193155/19.

Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a healthy subject.

Example 11; SEQ ID NO 663; 241pp; English.

The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level be marker gene in a biological sample from a subject, comparing the expression level a bronchial asthma or chronic expression levels increase when respiratory epithelial constructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) constructive pulmonary disease; (C) a kit for screening for bronchial asthma or chronic obstructive pulmonary disease; (C) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (C) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (C) a therapeutic agent for bronchial constructive pulmonary disease; (C) a therapeutic agent for bronchial constructive pulmonary disease; (C) a therapeutic agent for bronchial constructive pulmonary disease; (C) a therapeutic agent for bronchial constructive pulmonary disease; (C) a portion of the gene through an RNAi effect or an antibody recognising the expression of the gene through an RNAi effect or an antibody recognising constructive muchial asthma or a chronic obstructive pulmonary disease, (C) a probe has been immobilised to assay a marker gene. (I) has respiratory for probe the septivities, and can be used in gene through an experience of the marker gene. (I) has respiratory for and antiasthmatic activities, and can be used in gene through an experience of the marker gene. (I) and the probable of the marker gene. (I) and constitution of the and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.

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WPI; 2004-193155/19.
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                                                                           1 MALAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWRHFARKDLSEADARIF
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                                                                                                     KAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHK
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                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bronchial asthma; chronic obstructive pulmonary disease;
respiratory epithelial cell; interleukin-13; respiratory;
gene therapy; marker.
                            Length
                                              2; Indels
                                                                                                                                                                                          DLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAG-
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                           DB 8;
                          Score 2533.5; DB 8
Pred. No. 7.7e-182;
0; Mismatches 2;
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2003JP-00077212
                          Query Match 92.8%;
Best Local Similarity 93.8%;
Matches 472; Conservative
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          Sequence 474 AA;
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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises or chronic obstructive pulmonary disease. The method comprises correlating the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level be marker gene comprises (a) a group of carboric and judging whether the subject has bronchial athma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (51) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (52) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (52) whose expression levels decrease when respiratory epithelial are stimulated with interleukin-13. Also described: (l) a reagent (l) for certaing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mounes; (5) a marker gene or an annial model for bronchial asthma in a moune; (5) a sethma or chronic obstructive pulmonary disease, comprising the compound, a marker gene, an intisense mucleic acid corresponding to a portion of the marker gene or an antisense mucleic acid corresponding to a portion of the marker gene, a riboxyme, a polymucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising conchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (1) has respiratory and antiasthmatic activities, and can be used in gene therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present conchial asthma or chronic obstructive pulmonary disease. The present conchial asthma or chronic obs
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Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 ETTPSPGPQPAALTIGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTV
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                                                                                                                                                                                                                                         Example 11; SEQ ID NO 715; 241pp; English
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Best Local Similarity 93.8'
Matches 472; Conservative
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LRGPOLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRAR 391

LRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRAR

LOKVVGHPSCTFLYGPPDPAVRATDPQQVAFPSPABLPDQKQLRYTBBLLRHVAPGLHLB

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human cliagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnost e g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp inflammatory disorders, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D; Patury S, Shi X, Suarez CJ;
New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnostic a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
                                                                                                                                                                                                                                                                                                                                                          gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
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                                                                           CLSSANSLYDDIECFLMELEOPA
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N-PSDB; ACN41682.
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                                                              20 RAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVFWKHFARKDLSEADARIFKAWAVA
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                                              7 RAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVA
                                                                                                     67 RGRWPPSSRGGCPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSR
                                                                                                                                                                                         140 ELCWREGPGTDQTEAEAPAAVPPP-------
                                                                                                                                                                                                                                                                               GPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDUTIMYKGRTVLQKVVG
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gletzen
Patury S, Shi X, Suarez CJ;
                 Gaps
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                 Indels
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12-SEP-2002; 2002US-0410260P.
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A puricleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine cutoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the cinvention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                     New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosting a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
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                         WPI; 2004-329368/30.
N-PSDB; ACN41683.
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Sequence 440 AA;

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GPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVLOKVVG 244
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                                                                                                                                                                   RGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSR 126
                                                                                                                                                                                                          RGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSR 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 RYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSSLSLCLSSSN 423
                                                                                                                            20 RAAPRVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVA 79
                                                                                         7 RAAPRVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVA
                                                 16;
        80.9%; Score 2210; DB 8; Length 440; ilarity 84.1%; Pred. No. 1.4e-157; Conservative 0; Mismatches 3; Indels 7
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version - 2005
GenCore
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- protein search, using sw model protein May Run on:

6, 2005, 16:40:43 ; Search time 44 Seconds (without alignments) 853.375 Million cell updates/sec

US-09-647-965-9 2731

1 MALAPERAAPRVLFGEWLLG.......SANSLYDDIECFLMELEQPA 503 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 segs, 74649064 residues Searched:

513545 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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/cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\* Issued Patents AA:\* 4 0 0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 11716, A			8970,	8969,	6096,	7374	16, Ag	16,	2, 7	'n	ď	73	25	25,	25,	٠.	•	Sequence 29, Appl	٠.	٠,	~	٠.	Sequence 5, Appli		Sequence 2, Appli	Camping 7 April
SUMMARIES	ID	US-09-949-016-11716	US-08-999-774A-10	US-09-949-016-11715	US-09-949-016-8970	US-09-949-016-8969	US-09-949-016-6096	US-09-949-016-7374	8	US-09-417-540-16	US-08-611-280-2	US-09-195-940-2	US-09-562-466-2	US-09-949-016-7334	US-08-611-280-25	US-09-195-940-25	US-09-562-466-25	US-08-654-482-14	US-09-949-016-6229	US-09-230-371A-29	US-09-949-016-11483	US-09-230-371A-30	US-09-079-030-81	US-09-149-476-374	US-08-654-482-5	US-08-654-482-1	US-08-654-482-2	TTS-08-654-482-7
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do	Query Match	99.4	98.7	98.4	95.6	54.2	16.8	16.8	16.6	16.6	13.8	13.8	13.8	13.3	13.2	13.2	13.2	13.1	13.1	12.0	11.3	11.2	9.6	9.5	8.3	8.1	8.1	0
	Score	2715	2695	2686	2529.5	1479	458	458	454	454	376	376	376	363	361.5	361.5	361.5	357	357	328.5	308.5	306	270.5	259.5	228	222.5	222.5	210
	Result No.	-	7	е	4	ហ	φ	7	80	0	10	11	. 12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	22

Sequence 5424, Ap Sequence 6, Appli Sequence 5034, Ap Sequence 1930, Ap Sequence 25050, A Sequence 25050, A Sequence 11359, A Sequence 4, Appli Sequence 945, Appli Sequence 945, Appli	Sequence 13993, A Sequence 52, Appl Sequence 52, Appl Sequence 5, Appl Sequence 5, Appl Sequence 76, Appl Sequence 41, Appl Sequence 41, Appl
US-09-513-999C-5424 US-08-654-482-6 US-09-513-995-5034 US-09-949-016-6188 US-09-949-016-7930 US-09-949-016-11359 US-08-654-482-4 US-08-654-482-3 US-08-654-482-3	US-09-902-540-13993 US-09-949-016-9700 US-09-642-255-52 US-08-642-255-62 US-09-219-849-5 US-09-919-497-76 US-09-919-497-76 US-09-283-411 US-09-283-471A-41
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136 107 107 325 390 380 382 108 108	420 713 561 1064 960 349 355
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214 212 198.5 176 176 169.5 167 167 161.5	156.5 155.5 154.5 153.5 153.153
	. W W 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

#### ALIGNMENTS

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FAUCHING NO. SERVERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
SPIOR APPLICATION NUMBER: 60/231, 498
PRIOR FILING DATE: 2000-10-03
SPIOR APPLICATION NUMBER: 2000-10-03
SPIOR APPLICATION NUMBER: 50/0712
SPIOR APPLICATION NUMBER: 50/0712
SPIOR APPLICATION NUMBER: 50/0712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHK 120
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99.4%; Pred. No. 1.8e-224;
tive 1; Mismatches 2;
                    Sequence 11716, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 99.4
Matches 500; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Human
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US-09-949-016-11716
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301 LQKVVGHPSCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLE 360

DILIÇAVQQSCLADHLITASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAV 317

DLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAV

360 420

300

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Sequence 11115, Application US/09949016

Sequence 11115, Application US/09949016

GENERAL INFORMATION:
APPLICANT: VENTER, USTROPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPREMENCE: CLOOD1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSELSEQ for Windows Version 4.0

LENGTH: 538

LENGTH: 538
                                                                                                                                                                                                                                                    241 EKTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTV 300
                                                                                                                                                                                                                                                                                                                                                                                                  361 LRGPQLWARRWGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRAR 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 ORRGSPRYTIYLGFGODLSAGRPKEKSLVLVKLEPWLCRVHLEGTOREGVSSLDSSSLSL 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 VQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSP 246
  61 KAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHK 120
                                                                                                                                                    301 LQKVVGHPSCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLE
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                                          121 VYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKG
                                                                                 121 VYALSRELCWREGPGTDOTEAEAPAAVPPPOGGPPRPFLAHTPAGLOAPGPLPAPAGDKG
                                                                                                                            DLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAV
                                                                                                                                                                                                         ETTPSPGPOPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTV
                                                                                                                                                                                                                                                                                           LOKWYGHPSCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLE
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Pred. No. 4.9e-222;
1; Mismatches 2;
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Best Local Similarity 99.4%;
Matches 494; Conservative
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US-09-949-016-11715
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                         437
                                                                                                                                               QRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDL 480
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1 MALAPERAAPRVLFGEWILGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIF
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APPLICANT: Gish, Kurt C.
APPLICANT: Sephezi, Wolfgang
APPLICANT: Shanahan, Frances
APPLICANT: Lees, Emma M.
TITLE OF INVENTION: Intracellular Regulatory Molecules;
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Incre-
STREET: 901 Califa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 503;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
TLING DATE: 10-DEC-1997
CLASSIFICATION NUMBER: 08/08/99,774A
FILING DATE: 10-DEC-1997
CLASSIFICATION NUMBER: 08 60/032,818
APPLICATION NUMBER: 08 60/032,818
FILING DATE: 11-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/POCKET UNBER: 34,090
REFERENCE/POCKET UNBER: 22,096
TELEDPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2695; DB 3;
Pred. No. 7.6e-223;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: DNAX Research Institute STRET: 901 Callfornia Avenue CITY: Palo Alto STATE: California COUNTRY: USA ZIP: 94304-1104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                               CLSSANSLYDDIECFLMELEQPA 503
                                                                                                                                                                                                                                                        CLSSANSLYDDIECFLMELEQPA 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.0%;
Matches 498; Conservative
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MOLECULE TYPE: protein
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RESULT 5

US-09-949-016-8969

US-09-949-016-8969

Sequence 8969, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOU3307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2007012

SOFTWARE: PRESEED for Windows Version 4.0

LENGTH: 288
57 SPSPSACTAVQEPSPGALDVIIMYKGRTVLQKVVGHPSCTFLYGPPDPAVRATDPQQVAF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 PACLLPRNCDTPIFDFRVFFRELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLV
                                                                                                              469 QRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSSLSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 SPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVGHPSCTFLYGPPDPAVRATDPQQVAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 PSPAELPDOKQLRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               392 PACLLPRNCDTPIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLV
                                                                                                                                                                         QRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDL
                                                                                      LRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 278; Conserv
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US-09-949-016-6096
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Sequence 8970, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PLILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-00-08

PRIOR FILING DATE: 2000-00-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NOS: 207012

SEQ ID NO 8970
                                                                                                                                                 VYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGFFLAHTHAGLQAPGFLPAPAGDKG 180
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Matches 471; Conservative
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR PLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-06
RIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FARENCE for Windows Verbion 4.0
SEC ID NO 6096
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Betent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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16.8%; Score 458; DB 4; Length 427;
Best Local Similarity 28.0%; Pred. No. 4.7e-31;
Matches 141; Conservative 64; Mismatches 191; Indels 108;
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28.0%; Pred. No. 4.9e-31;
ive 64; Mismatches 191; Indels 108;
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APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
APPLICANT: Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
TITLE OF INVENTION: Expression Products
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STRAET: NEW JERSEY
COUNTRY: USA
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                         PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7374
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APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/08705771
Patent No. 6054289
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 28.08
Matches 141; Conservative
                                                                                                                                                                                                                                                                                  ORGANISM: Human
                                                                                                                                                                                                                                                                                                            US-09-949-016-7374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 PRVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVARGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 YVP----GRDKPDLPT----WKRNFRSALNRKEGLRLAEDRSKDPHDPHKIYEFV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 16.6%; Score 454; DB 4; Length 427; Best Local Similarity 28.0%; Pred. No. 1e-30; Matches 141; Conservative 63; Mismatches 192; Indels 108; Gaps
CECCHI, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD CITY: ROSELAND STATE: NEW JERSEY COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGIGTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/417,540 FILING DATE: 14-Oct-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                  ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: WORD PERPECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/705,771
FILING DATE: August 30, 1996
ATTORNEY/AGENT INFORMATION:
NAME: WULLINS, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       479 DLCLSSANSL --- YDDIECFLMEL 499
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 WREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQ 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 EDILDELL-GNMVLAPLP------DPGPP-----SLAVAPEPCPO 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 PAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEP-SPGALDVTIMYKGRTVLQKVVGHP 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 16.6%; Score 454; DB 3; Length 427; Best Local Similarity 28.0%; Pred. No. 1e-30; Matches 141; Conservative 63; Mismatches 192; Indels 108;
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Jian Ni and Jing-Shan Hu
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                                                                                                                                                                                                                                                                              325800-346 (PF196)
                            COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,771
FILING DATE: AUGUST 30, 1996
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 -NSGVG----DFSQPDTSPDTNGG
                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
                                                                                                                                                                                                                                                                                                                                                TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                           : 427 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-705-771-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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US-09-417-540-16
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75 RGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREG 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTPSPG-PQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----RLHICLYKRDILV 263
  318 WMAPDGLYAKRLCQSRIYWD--GPLALCSDRPNK----LERDQTCKLFDTQQFLSELQVF 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 EWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Grossman, Alex
APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
CORRESPONDENCE ADDRESS: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.8%; Score 376; DB 3; Length 450; 28.1%; Pred. No. 5.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                     - AHHGRPAPRFQVTLCFGEEFPDPQ-RQRKLITAHVEPLLAR 411
                                            418 RARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---DSDC---
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                                                                                                                                                                                                                                                                                                                                                                                      E: Amgen Canada Inc.
6733 Mississauga Road, Suite 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/611,280
                                                                                                                                                                                           Sequence 2, Application US/09195940
Patent No. 6258935
GENERAL INFORMATION:
                                                                                                                                                                                                                                                           APPLICANT: Matsuyama, Toshifumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-3
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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227 ESQAPGIPIEPSIRSAEALA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 28.19
Matches 130; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Mississauga
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 LOKVVGHP-SCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTBELLRHVAPGLHL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 KELTITSPEGCRISHG---HYYDVSNLDQVLFPYP---DDNGQRKNIEKLLSHLERGLVL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 ELRGPQLWARRMGKCKVYWEVGGPPGSAS -- PSTPACLLPRNCDTPIFDFRVFFQELVEF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 RGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREG 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 MMPPH--DRSW-RDYAPDQSHPEIPYQCPVTFGPRGHHWQGPSCENGCQVTGTFYACAPP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 ESQAPGIPIEPSIRSAEALA------LSDC------RLHICLYYRDILV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 EWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS 74
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                                                                                                                                                APPLICANT: Grossman, Alex
APPLICANT: Grossman, Alex
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen C.-..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.8%; Score 376; DB 2; Length 45:
28.1%; Pred. No. 5.4e-24;
tive 66; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,280
                                                                                                                                                                                                                                                                                                                        E: Amgen Canada Inc.
6733 Mississauga Road, Suite 303
|| :|::: | : | :| :| DLHISNSHPLSLTSDQYKAYLQDL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Matsuyama, Toshifumi, APPLICANT: Grossman, Alex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-33:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               450 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: Canada
ZIP: LSN 6JB
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                CITY: Mississauga
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Matches 130; Conserv
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Sequence 7334, Application US/09949016
Patent No. 681239
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,468
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 -GAKQLTLEDPQM------SMSHPYT-MTTPYPSLPA------QQVHNYMM 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 MMPPH--DRSW-RDYAPDQSHPEIPYQCPVTFGPRGHHWQGPSCENGCQVTGTFYACAPP 226
                                                                TIPSPG-POPAALTIGEAAAPESPHOAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRIV 300
                                                                                                                                                                                 264 KELTITSPEGCRISHG---HTYDVSNLDQVLFPYP---DDNGQRKNIEKLLSHLERGLVL 317
                                                                                                                                                                                                                                                  ELRGPOLWARRMGKCKVYWEVGGPPGSAS -- PSTPACLLPRNCDTPIFDFRVFFQELVEF 417
                                                                                                                                                                                                                                                                               318 WMAPDGLYAKRLCQSRIYWD--GPLALCSDRPNK----LERDQTCKLFDTQQFLSELQVF 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADHLLTASWGADPVPTKAPGEGQEGLPLT------GACAGGPGLPAGELYGWAVET 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 PP--LDRSW-RDYVPDQPHPEIPYQCPMTFGPRGHHWQGPACENGCQV-TGTFYACAPPE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 TPSPG-PQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVL 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 RGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREG
                                                                                                         -----BDC-----RLHICLYYRDILV
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                                                                                                                                                         301 LOKVVGHP-SCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHL
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                                                                                                                                                                                                                                                                                                                                                RARORRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCR 459
                                                                                                                                                                                                                                                                                                                                                                           372 -AHHGRPAPRFQVILCFGEEFPDPQ-RQRKLITAHVEPLLAR 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.3%; Score 363; DB 4; Lu
Best Local Similarity 27.5%; Pred. No. 7.9e-23;
Matches 136; Conservative 73; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7334
                                                                                                              227 ESQAPGIPIEPSIRSAEALA
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-7334
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  LQKVVGHP-SCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHL 359
                            264 KELTTISPEGCRISHG---HTYDVSNLDQVLFPYP---DDNGQRKNIEKLLSHLERGLVL 317
                                                                                           417
                                                                                                                   RGGGPPFEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREG 133
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                                                                                           360 ELRGPQLWARRMGKCKVYWEVGGPPGSAS--PSTPACLLPRNCDTPIFDFRVFFQELVEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 REGIDKPDPPT-----WKTRLRCALNKSNDFEELVERSQLDISDPYKVYRI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.8%; Score 376; DB 3; Length 450; 28.1%; Pred. No. 5.4e-24;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/562,466
FILING DATE: 01-May-2000
CLASSIFICATION: <UNKNOWID>
                                                                                                                                                                                    418 RARQRRGSPRYTIYLGFGODLSAGRPKEKSLVLVKLEPWLCR 459
                                                                                                                                                                                                              Query Match
13.8%; Score 376; DB
Best Local Similarity 28.1%; Pred. No. 5.4e
Matches 130; Conservative 66; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: <URKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-338A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-562-466-2
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APPLICATION NUMBER: 09/195,940
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Matsuyama, Toshifumi
Grossman, Alex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09562466
Patent No. 6369202
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Mississauga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: Canada
ZIP: L5N 6JB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Ontario
                                                                                                                                                                                                                                                                                                     RESULT 12
US-09-562-466-2
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Db 225 PESQAPGUPTEPSIRSAEALAFSDCRLHICLYYREIL 261  QY 300 VLQKVVGHP-SCTFLYGPPDPAVRATDDQQVAFPSPAELDDGKQLRYTEELLRHYAPGLH 358		Patent No. 6258935   GENERAL INFORMATION:   APPLICANT: Mateuyama, Toshifumi   APPLICANT: Grossman, Alex   APPLICANT: Grossman, Christopher D.   APPLICANT: Richardson, Christopher D.   TITE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES   NUMBER OF SEQUENCES: 25   CORRESPONDENCE ADDRESS:   ADDRESSEE: Amgen Canada Inc.   STREET: G733 Mississauga Road, Suite 303   STATE: Ontario   STATE: Ontario	N 6JB EADABLE FORM: YPE: IBM PC COMING SYSTEM: PC. PATE: PATENT R PLICATION DATE: CATION: CATION: CATION: CATE: CATION: CATE: CA	REGISTRATION NUMBER: 34,688  REFERENCE/DOCKET NUMBER: A-338A  INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS: LEMOTH: 450 amino acids  TYPE: amino acid STRANDEDNES: single COCLUCY: linear MOLECULE TYPE: protein US-09-195-940-25	Query Match       13.2%;       Score 361.5;       DB 3;       Length 450;         Best Local Similarity       27.2%;       Pred. No. 9.6e-23;       Antoles       194;       Indels       97;       Gaps       22;         Qy       16       EWLIGBISSGCYEGLQWLDEARTCFRVPWKHFARKDLS-EADARIFKAMAVARGRWPPSS       74
Qy         361 LRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFR 418           Db         354 MAPDGLYAKRLCQSRIYWDGPLALCNDRPNKLERDQTCKLFDTQQFLSELQAF- 406           Qy         419 ARQRRGSPRYTTYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDL 478           Db         407 AHHGRSLPRFQVTLCFGBEFPDPQ-RQRKLITAHVEPLLARQLYYFAQQNSGHFLRGYDL 465           Qy         479 DLCLSSANSLYDDI 492           Db         466 PEHISNPEDYHRSI 479	RESULT 14 US-08-611-280-25 ; Sequence 25, Application US/08611280 ; Parent No. 5891666 ; GENERAL INFORMATION: ; APPLICANT: Matsuyama, Toshifumi ; APPLICANT: Grossman, Alex ; TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES ; NUMBER OF SEQUENCES: 25	CORRESPONDENCE ADDRESS:  HODRESSEE: Angen Canada Inc. STREET: 6733 Mississauga Road, Suite 303 CITY: Mississauga Road, Suite 303 STATE: Ontario CONTRY: Canada CIP: LSN 6JB COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:	APPLICATION NUMBER: US/08/611,280 FILING DATE: CLASSIFICATION: 415 CLASSIFICATION: 415 ATTORNEY/AGENT INFORMATION: NAWE: Oleski, Nancy A.; REGISTRATION NUMBER: 34,688 REFERENCE/DOCKET NUMBER: 34,688 REPERENCE CHARACTERISTICS: LENGTH: ACO maino acids TYPE: anino acid TYPE: anino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein US-08-611-280-25	Query Match Best Local Similarity 27.2%; Pred. No. 9.6e-23; Matches 135; Conservative 70; Mismatches 194; Indels 97; Gaps 22;  Qy 16 EWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWFPSS 74  :     :	82 REGIDKPDPPTWKTRLRCALNKSNDFBELVERSQLDISDPYKVYRIVPEGAKK 134 PGTDQTEAEAPAAVPPPQGGPPGPFL-AHTHAGLQAPGPLPAPAGDKGDLLLQAVQQS 135 -GAKQLTLEDPQMSMSHPYTWTTPYPSLPAQVHNYMMPP

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134 PGTDQTEAEAP--AAVPPPQGGPPGPFL-AHTHAGLQAPGPLPAPAGDKGDLLLQAVQQS 190
                     135 -GAKQLTLEDPQMSMSHPYTWTTPYPSLPAQVHNYMMPP---------172
                                                191 CLADHLLTASWGADPVPTKAPGEGQEGLPLT-----GACAGGPGLPAGELYGWAV 240
                                                               173 -----LDRSW-RDYVPDQPHPEIPYQCPMTFGPRGHHWQGPACENGCQV-TGTFYACAP 224
                                                                                                 241 ETTPSPG-PQPAALITGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRT 299
                                                                                                                    300 VLQKVVGHP-SÇTFLYGPPDPAVRATDPQQVAFPSPABLPDQKQLRYTEBLLRHVAPGLH 358
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May 6, 2005, 16:44:59 ; Search time 58 Seconds (without alignments) 2893.107 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                               1428581 seqs, 333598853 residues
                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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2731
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PUDILIBREA APPLICATIONS AND TO THE COME. PROPERTY CONTROL OF CONTR Applications AA: Published Database :

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

seq length: 0 seq length: 200000000

Minimum DB Maximum DB M

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1291, App Sequence 1293, App Sequence 2, Appli Sequence 16, Appli Sequence 16, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 1292, Ap Sequence 1292, Ap Sequence 356, App Description US-09-975-253-2 US-09-975-253-2 US-09-975-253-2 US-10-264-049-4045 US-10-840-139B-2 US-10-840-139B-3 US-10-744-600-1292 US-10-492-043-2 US-10-492-043-30 US-10-755-889-356 US-10-741-600-1291 US-10-741-600-1293 SUMMARIES Query Match Length DB Score 335.55 Result 8

RUWWWU10044444000044446444	47.4 7.4 7.7
US-10-492-043-5 US-10-276-774-2333 US-09-802-31-374 US-09-802-31-374 US-10-164-861-374 US-10-164-861-374 US-10-264-049-229 US-10-264-049-229 US-10-108-260A-4496 US-10-901-816A-12 US-10-901-816A-12 US-10-901-816A-12 US-10-901-816A-12 US-10-901-816A-12 US-10-901-816A-12 US-10-35-569A-4 US-10-35-569A-4 US-10-35-569A-4 US-10-36-391-34 US-10-36-391-34 US-10-3431-3 US-10-342-331-5 US-10-402-099-4 US-10-402-099-4 US-10-402-099-4 US-10-402-099-6 US-10-402-099-6 US-10-402-099-6 US-10-402-099-6	US-10-437-963-162013 US-10-437-963-187017 US-09-976-740-47 US-10-023-529-47 US-10-023-523-47
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328.5 329.5 259.5 259.5 188.5 170 171 166.5 157 157 158 158 158 158 158 158 158 158 158 158	151 151 150.5 150.5
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## ALIGNMENTS

NF-kB

RESULT US-10-	RESULT 1  US-10-755-889-356  Publication No. US20040171823A1  Sequence 356, Application uS/10755889  Publication No. US20040171823A1  GENERAL INFORMATION:  APPLICANT: Bristol-Hyers Squibb Company  TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-1  TITLE OF INVENTION: PATHWAY  FILE REFERENCE: DO284 NP  CURRENT APPLICATION NUMBER: US. 60/440,068  PRIOR PILING DATE: 2003-01-13  PRIOR PILING DATE: 2003-05-12  NUMBER OF SEQ ID NOS: 823  SOFTWARE: Patentin version 3.2  SEQ ID NO 356  LENGTH: 164  TYPE: PRI  TYPE
Quer Best Matc	Query Match Best Local Similarity 100.0%; Pred. No. 1e-50; Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
è 6	1 MALAPERAAPRVLFGEWLIGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIF 60
& <u>a</u>	61 KAWAVARGEWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRFFVMLRDNSGDPADPHK 120 

121 VYALSRELCWREGPGTDQTEAEAPAAVPPQ 151

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GENERAL INFORMATION:
APPLICANT: Paul Moore et al.
TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Infection
TITLE OF INVENTION: Using Human Interferon Regulatory Factor 3
TITLE OF INVENTION: Using Human Interferon Regulatory Factor 3
TITLE OF INVENTION: Using Human Interferon Regulatory Factor 3
TITLE OF INVENTION: Using Human Interferon Regulatory Factor 3
CURRENT APPLICATION NUMBER: US/09/975,253
CURRENT FILING DATE: 2001-10-12
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 WREGPGTDQTEAEAPAAVPPPQGGPPGFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --GSTSD----TQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 EGLRLVG-SEVGDRTLPGWPVTLPDPGMSLTDRGVMSYVRHVLSCLGGGLALWRAGQWLW 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 PAALTIGEAAAPESPHQAEPYLSPSPSACTAVQEP-SPGALDVTIMYKGRTVLQKVVGHP 308
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                                                                                                                                                                                                                                                                                            Indels 108;
                                                                                                                                                                                                                                             16.8%; Score 458; DB 17; 28.0%; Pred. No. 5.6e-24; iive 64; Mismatches 191;
                                                 NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1293
    CURRENT APPLICATION NUMBER: US/10/741,600
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Patent No. US20020164694A1
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Best Local Similarity 28.0
Matches 141; Conservative
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SEQ ID NO 2
LENGTH: 427
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CRGANISM: Homo sapiens
US-10-741-600-1293
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FEATURE:
NAME/KEY: misc_feature
                             CURRENT FILING DATE:
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                                                                                                                          LENGTH: 427
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Publication No. US20050026169A1
GENERAL INFORMATION:
TITLE OF INVENTION: Michele et al.
TITLE OF INVENTION: MOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001499
                                                                                                                                                                                                                 APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO4499
CURRENT APPLICATION NUMBER: US/10/741,600
KURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: PASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSRELC 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.8%; Score 458; DB 17; Length 427; 28.0%; Pred. No. 5.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64; Mismatches 191;
DLCLSSANSL ---YDDIECFLMEL 499
                                                                                                                                           ; Sequence 1291, Application US/10741600; Publication No. US20050026169A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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130 WREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQ 189
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                                                                                       WPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSRELC 129
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  PRVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVARGR
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REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
TELECOMMUNICATION INFORMATION:
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CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
Expression Products
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COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,478
FILING DATE: 04-Jun-2003
CLASSIFICATION: 536
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- APPLICATION NUMBER: US/08/705,771
FILING DATE: AUGUSE 30, 1996
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                              Query Match 16.6%; Score 454; DB 9; Length 427; Best Local Similarity 28.0%; Pred. No. 1.1e-23; Matches 141; Conservative 63; Mismatches 192; Indels 108;
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  or Val
; OTHER INFORMATION: Xaa equals 11e, Leu, Phe, US-09-975-253-2
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/239,963
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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Publication No. US20050054033A9
GENERAL INFORMATION:
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Matches 141; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 427
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                                                                                                                                                                                         ; Score 454; DB 15; Length 427;
; Pred. No. 1.1e-23;
63; Mismatches 192; Indels 108;
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Fublication No. US20040005579A1
GENERAL INFORMATION:
ADDICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PA139P1
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: US/10/264,049
PRIOR APPLICATION NUMBER: PT/US01/18569
PRIOR PILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
NUMBER OF SEQ ID NOS: 4360
                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
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                                 SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
TELEFAX: 973-994-1744
               INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                         Query Match
Best Local Similarity 28.0%;
Matches 141; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 EDILDELL-GNMVLAPLP
                                                                         TYPE: amino acid
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NAME/KEY: MISC_FEATURE
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occurring L-amino acids
                                                                                                         twenty naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids US-10-264-049-4045
                                                                                                                                                                                                                                                                                                                                  L-amino acide
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APPLICANT: Murray, Jeffrey C.
APPLICANT: Murray, Jeffrey C.
APPLICANT: Morndo, Shinji
APPLICANT: Morndo, Shinji
APPLICANT: Dixon, Michael J.
TITLE OF INVENTION: IRF6 POLYMORPHISMS ASSOCIATED WITH CLEFT LIP AND/OR PALATE
FILE REPERENCE: P06215US01
CURRENT PAPLICATION NUMBER: US/10/840,139B
CURRENT FILING DATE: 2004-05-06
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 4
SOCTWARE: PATENTIN NOS: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422 RRGSPRY-TIY----LGFGQDLSAGRPKEK-----SLVLVKLEPWLCRVHLEGTQREG 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ELVEFRARQ 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||
62 CLLPRNCDTPIFDFRVFFQGQVRPLAMGXGFKGSLGKHLPCQVLXKKSPSSELVEF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 PAELPDOKOLRYTEELLRHVAPGLHLELRGPOLWARRMGKCKVYWEVGGPPGSASPSTPA
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                                                                                                                                                                                                                                                                                                                                  occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58;
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OTHER INFORMATION: Xaa equals any of the twenty naturally
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                                                                                                                                                                                                                                                                                                                                  twenty naturally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 446; DB 15;
Pred. No. 1.4e-23;
9; Mismatches 16;
                                                                                                         OTHER INFORMATION: Xaa equals any of the
                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa equals any of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 CLLPRNCDTPIFDFRVFFQ-------
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Best Local Similarity 55.1%;
Matches 102; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                            FEATURE:
NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                                                                            NAME/KEY: MISC_FEATURE
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                                                                                                                                                               NAME/KEY: MISC_FEATURE
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Matches 142; Conserv
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NAME KEY: VARIANT
LOCATION: (70)..(70)
OTHER INFORMATION: Gly70Arg
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OTHER INFORMATION: ASP98His
FEATURE:
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OTHER INFORMATION: His156fs
                                          LOCATION: (18)..(18)
OTHER INFORMATION: Val18Met
                                                                                                                                                                                                                                                                                                                                         LOCATION: (39)..(39)
OTHER INFORMATION: Pro39Ala
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THER INFORMATION: Lys89Glu
FEATURE:
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LOCATION: (90)..(90)
OTHER INFORMATION: Ser90Gly
FEATURE:
                                                                                                                                                   NAME/KEY: VARIANT
LOCATION: (18)..(18)
OTHER INFORMATION: Vall8Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (60)..(60)
OTHER INFORMATION: Trp60Gly
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OTHER INFORMATION: Ala61Gly
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LOCATION: (66)..(66)
OTHER INFORMATION: Lys66Thr
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THER INFORMATION: Pro76Ser
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THER INFORMATION: GIN82Lys
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THER INFORMATION: Arg84Cys
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THER INFORMATION: Arg84His
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OTHER INFORMATION: Gln118X
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LOCATION: (92)...(92)
OTHER INFORMATION: Glu92X
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THER INFORMATION: Gln68X
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NAME/KEY: VARIANT
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NAME/KEY: VARIANT
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NAME/KEY: VARIANT
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AME/KEY: VARIANT
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       NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10840139B
Publication No. US20050089865A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL Schutte, Brian C.
APPLICANT: Schutte, Brian C.
APPLICANT: Schutte, Dixon, Michael J.
TITLE OF INVENTION: RF6 POLYMORPHISMS ASSOCIATED WITH CLEFT LIP AND/OR PALATE TILE REFERENCE: D621510501
CURRENT APPLICATION NUMBER: US/10/840,139B
CURRENT PILING DATE: 2004-05-06
RIOR PELING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.3
08 VKIY----QVC-----DIPQPQPQG-----SIINPGSTGSAPWD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 ---W-----PKTEPLEMEVPQ--APIQPFYSSPELWISSLPMT------DLDIKFQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 YKGRTVLOKV-VGHP-SCTFLYGPPDP-----AVRATDPQQVAFPSPAELPDQKQLRYT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 YRGKEYGQTMTVSNPQGCRLFYGDLGPMPDQEELFGPVSLEQVKPFGPEHITNEKQKLFT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 LETFLSDLIAHQKGQIEKQPPFEIYLCFGEEWPDGKPLERKLILVQVIPVVARMIYEMFS 407
                                                                                                                    119 HKVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGD 178
                                                                                                                                                                                                                                                                   179 KGDLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPL----TGACAGGPGLPAGE 234
                                                                                                                                                                                                                                                                                                                                         136 EKD---NDVDEEDEEDE-LDQSQHHVPIQDTFPFLNINGSPMAPASVGNCSVGNCSPEAV 191
                                                                                                                                                                                                                                                                                                                                                                                                                  235 LYGWAVETTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIM 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 EELLRHVAPGIHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFD 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407 FRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQ 466
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LOCATION: (1)..(1)
OTHER INFORMATION: Metille
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NAME/KEY: VARIANT
LOCATION: (2)..(2)
OTHER INFORMATION: Ala2Val
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LOCATION: (17)..(17)
JTHER INFORMATION: Gln17fs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC_FEATURE
OTHER INFORMATION: 5' UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT
LOCATION: (6)..(6)
OTHER INFORMATION: Argéfs
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LENGTH: 467
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-840-139B-3
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OCATION: (297)..(297)
THER INFORMATION: Val2971le
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OTHER INFORMATION: Leu345Pro
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OTHER INFORMATION: Phe369Ser
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THER INFORMATION: Arg250Gln
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THER INFORMATION: Gln273Arg
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THER INFORMATION: Val2741le
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INFORMATION: Leu294Pro
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THER INFORMATION: LY8320Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COCATION: (321)..(321)
THER INFORMATION: Val321Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COCATION: (325)..(325)
THER INFORMATION: Gly325Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (347)..(347)
OTHER INFORMATION: Cys347Phe
                                                                                                                                                                                                                   AAME/KEY: VARIANT
COCATION: (219) ..(219)
THER INFORMATION: Ser219fs
                                                                                                                                                                LOCATION: (212)..(212)

THER INFORMATION: Ser212fs
                                                                                                                                                                                                                                                                                                                           OCATION: (248)..(248)
THER INFORMATION: Gly248fs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OCATION: (265)..(265)
THER INFORMATION: Leu265fs
LOCATION: (186)..(186)

STHER INFORMATION: Cys186X
                                                                                COCATION: (192)..(192)
THER INFORMATION: Trp192X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
LOCATION: (253)...(253)
THER INFORMATION: TYr253X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (374)..(374)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
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                                                                                                                                           NAME/KEY: VARIANT
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Sequence 1222, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:
TUTLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION UNMER: US/10/741,600
CURRENT FILING DATE: 2003-12-2
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: PEASESQ for Windows Version 4.0
SEQ ID NO 1292
LENGTH: 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 FKAWAVETGKY---QEGVDDPDPAK-----WKAQLRCALNKSREFNLMYDGTKEVPMNP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 HKVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 LYGWAVETTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIM 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            407 FRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQ 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 FKAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGD-PADP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 VKIY----QVC-------DIPQPQG-------SIINPGSTGSAPWD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 KGDLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPL----TGACAGGPGLPAGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 ---W------PKTEPLEMEVPQ--APIQPFYSSPELWISSLPWT-------DLDIKFQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 YKGRTVLOKV-VGHP-SCTFLYGPPDP-----AVRATDPQQVAFPSPAELPDQKQLRYT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 EELLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFD 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MALAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFAR-KDLSEADARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 15.8%; Score 431; DB 17; Length 4 Best Local Similarity 27.7%; Pred. No. 4.9e-22; Matches 142; Conservative 72; Mismatches 211; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467 REGVSSLDSSDLDLCLSSANSLYDDIECFLMEL 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | | | : | : | : | : | : | : | 408 GDFTRSFDSGSVRLQISTPD-IKDNIVAQLKQL 439
                                                                              LOCATION: (388) .. (388)
OTHER INFORMATION: Lys388Glu
OTHER INFORMATION: Cy8374Trp
                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: VARIANT
LOCATION: (412)...(412)
OTHER INFORMATION: Arg412X
                                                                                                                                                                                            LOCATION: (393)..(393)
OTHER INFORMATION: Gln393X
                             FEATURE:
NAME/KEY: VARIANT
LOCATION: (388)...
                                                                                                                                           FEATURE:
NAME/KEY: VARIANT
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Sequence 1410, Application US/10276774

Sequence 1410, Application US/10276774

Publication No. US20040053245A1

GENERAL INFORMATION:

APPLICANT: Hang, Y. Tom et al

TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-030

CURRENT FILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: 09/560,875

PRIOR APPLICATION NUMBER: 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SOFTWARE: Custom

SEQ ID NO 1410
                                                                                                                                                                                  196
                                                                                                                                                                                                                                                                   T-----EAPFGGDQRSLEFILDP------PEPDXSLLLTFIYNGRVVGEAQVQSLD 240
                                                                              -----RQHSSVS----SERKEEED----AMQNCTLSP 156
                                                                                                                                                                                                                                     TGEAAAPESPHQAE----PYLSPSPSACTAVQEPSPG-ALDVTIMYKGRTVLQKVVGHPS 309
                                                                                                                                                                                                                                                                                                                                         310 CTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQLWAR 369
                                                                                                                                                                                                                                                                                                                                                                                    241 CRLV---AEPSGSESSMEQVLFPKPGPLEP-----TORLLSQLERGILVASNPRGLFVQ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                               RMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRG-SPRY 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 QVTLNFWEESHGSSHTPQNLITVKMEQAFARYLLEQTPEQQAAILSLVGPELESVLES 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   429 TIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGT--QREGVSSLDSSDLDLCLSS 484
                             GTDOTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQSCLAD
                                                                                                                              HLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQPAALT
                                                                                                                                                                                  157 SVLQDSLNNEE------EGASG----GAVHSDIG-----SSSSSSSPEPQEVTDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 GGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQSCLADHLLTASWGA-DPVPTKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGPPGFFLAHTHAGLQAPGPLLAPAGDEGDLLLLAVQQSCLADHLLTASWGGKDPIPTKA
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Publication No. US20050019306A1
GENERAL INFORMATION:
ADPLICANT: MOUNT SINAI SCHOOL OF MEDICINE OF NEW YORK UNIVERSITY
TITLE OF INVENTION: A HYBRID FUSION PROTEIN TRANSCRIPTION REGULATOR?
TITLE OF INVENTION: INDUCE INTERFERON TARGET GENE EXPRESSION
FILE REPERENCE: 4225-4000PC
CURRENT APPLICATION NUMBER: US/10/492,043
CURRENT FILING DATE: 2004-04-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LGEGOEGLPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 PGEGQEGLPLT
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Matches 64; Conserv
                                                                                125 GTQKVPSK-
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                                                                                                                                                                                                                                                                                   70 WPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSRELC 129
                                                                                                                                                                                                                                                                                                                      130 WREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                          11 -NSGVG----DFSQPDTSPDTNGG-----TO 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 SCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---DPGPP----SLAVAPEPCPQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 PAALTIGEAAAPESPHQAEPYLSPSPSACTAVQEP-SPGALDVTIMYKGRIVLQKVVGHP 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : : | | | | | : : | | | | | 1.0 PLRSPSLDNPTP-----FPNLGPSENPLKRLLVPGEEWEFEVTAFYRGRQVFQQTISCP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 SCTFLYGPPDPAVRATDPQQVAFPSPA-ELPDQKQLRYTEELLRHVAPGLHLELRGPQLW 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 EGLRLVG-SEVGDŘTLPGWPVTLPDPGMSLTDRGVMSÝVRHVĽSCLGGGLALWRAGOWLW 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 -----KEGDIGGPAVWKTRLRCALNKSSEPKEVPERGRMDVAEPYKVYQLLPPGIVSGQP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                  69
                                                                                                                                                                                                          APPLICANT: MOUNT SINAI SCHOOL OF MEDICINE OF NEW YORK UNIVERSITY
TITLE OF INVENTION: A HYBRID FUSION PROTEIN TRANSCRIPTION REGULATOR TO
TITLE OF INVENTION: INDUCE INTERFERON TARGET GENE EXPRESSION
CURRENT APPLICATION NUMBER: US/10/492,043
CURRENT PILING DATE: 2004-04-05
PRIOR PRIOR PRILING DATE: 2004-01-29
PRIOR PRILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PALCHIN VOIL 2.1
SEQ ID NO 2
LENGTH: 497
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                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 ARRMGKCKVYWEVG-----GPPGSASPSTPACLLPRNCDTPIFDFRVF 410
                                                                           Query Match 13.3%; Score 364.5; DB 17; Length 452; Best Local Similarity 27.4%; Pred. No. 2.2e-17; Matches 113; Conservative 43; Mismatches 153; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: P48-S2C protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 EDILDELL-GNMVLAPLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10492043 Publication No. US20050019306A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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; ORGANISM: Homo sapiens
US-10-741-600-1292
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US-10-492-043-2
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TYPE: PRT
ORGANISM: Homo sapiens
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   SEQ ID NO 5
LENGTH: 393
                                                                           US-10-492-043-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 SVLQDSLNNEE-----EGASG----GAVHSDIG-----SSSSSSSPEPQEVTDT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGEAAAPESPHQAE----PYLSPSPSACTAVQEPSPG-ALDVTIMYKGRTVLQKVVGHPS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 T-----EAPFQGDQRSLEFLLP-----PEPDYSLLLTFIYNGRVVGEAQVQSLD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 CTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQLWAR 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     429 TIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGT--QREGVSSLDSSDLDLCLSSAN 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/10492043
; Publication No. US20050019306A1
; GENERAL INFORMATION:
APPLICANT: WOUNT SINAI SCHOOL OF MEDICINE OF NEW YORK UNIVERSITY
TITLE OF INVENTION: A HYBRID FUSION PROTEIN TRANSCRIPTION REGULATOR TO
TITLE OF INVENTION: INDUCE INTERFERON TARGET GENE EXPRESSION
FILE REFERENCE: 4225-4000PC
CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: 60/352,777
PRIOR APPLICATION NUMBER: 60/352,777
PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 WLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSE-ADARIFKAWAVARGRWPPSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQPAALT
                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: p48-VP16 protein sequence
                                                                                                                                                                                                                                                                                 Length 473;
                                                                                                                                                                                                                                                                             12.2%; Score 332.5; DB 17; Length
25.6%; Pred. No. 4.1e-15;
tive 73; Mismatches 189; Indels
PRIOR APPLICATION NUMBER: 60/352,777
PRIOR FILING DATE: 2002-01-29
PRIOR PILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 30
LENGTH: 473
                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                Best Local Similarity 25.6%
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLYDD 491
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Sequence 2333, Application US/10276774
; Sequence 2333, Application US/2040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVERTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; TITLE OF INVERTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; TITLE OF INVERTION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Cuscom
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                                                                                                                                                                                                                                                                                  76 GGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREGP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 HLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQPAALT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 TGEAAAPESPHQAE----PYLSPSPSACTAVQEPSPG-ALDVTIMYKGRTVLQKVVGHPS 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 RMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRG-SPRY 428
                                                                                                                                                                                                                                                                                                                                                                                                                       135 GTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQSCLAD 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 CRLV---AEPSGSESSMEQVLFPKPGPLEP-----TQRLLSQLERGILVASNPRGLFVQ 291
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                                                                                                                                                                                ----KEGDIGGPÁVWKÍTRLRCALNKSSEFKEVPERGRMDVÁEPYKVÝQLLPPGIVSGQP
                                                                                                                                         17 WLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSE-ADARIFKAWAVARGRWPPSSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 112; Gaps
                                                                        66
       DB 17; Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   429 TIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGT--OREGVSSL 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 QVTLNFWEESHGSSHTPQNLITVKMEQAFARYLLEQTPEQQAAILSL 392
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Query Match 12.0%; Score 328.5; DB 17; Length Best Local Similarity 25.7%; Pred. No. 6.3e-15; Matches 120; Conservative 69; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.7%; Score 320; DB 15; Best Local Similarity 26.0%; Pred. No. 2.5e-14; Matches 119; Conservative 51; Mismatches 176;
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122 YALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLFAPAGDKGD 181	182 LLLQAVQOSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVE 241	242 TTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEF-SPGALDUTIMYKGRTV 300 242 TTPSPGPQPLRSPSLDNPTPPPNLGPSENPLKRLLVPGEEWEFEVTAFYRGRQV 174	301 LOKVVGHPSCTFLYGPPDPAVRATDPQQVAFPSPA-ELPDQKQLRYTEELLRHVAPGLHL 359 	360 ELKGPQLWARRMGKCKVYWEVGGPPGSASPSTFACLLPRNCDTPIFDFRVF 410	411 FQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEG 464 285 IVGSLGPPDLITFTEGSGR-SPRYALWFCVGESWPQDQPWTKRLVMVKVVPTCLRALVEM 343	465 TQREGVSSLDSSDLDLCLSSANSLYDDIECFLMEL 499 :           ::::     :::     :::   344 ARVGGASSLENT-VDLHISNSHPLSLTSDQYKAYLQDL 380	
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Search completed: May 6, 2005, 16:50:52 Job time : 60 secs

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Compugen Ltd.
version 5
- 2005 C
GenCore (c) 1993
       Copyright
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- protein search, using sw model OM protein May Run on:

6, 2005, 16:28:18 ; Search time 41 Seconds (without alignments) 1180.415 Million cell updates/sec

US-09-647-965-9

2731 1 MALAPERAAPRVLFGEWLLG......SANSLYDDIECFLMELEQPA score: Perfect so Sequence:

503

0.5 BLOSUM62 Gapop 10.0 , Gapext Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* ..... Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	interferon regulat	interferon regulat	interferon regulat	lymphoid-specific	interferon consens	transcription fact	interferon consens	transcription fact	<ul> <li>lymphoid-specific</li> </ul>	probable multi-dom	interferon regulat	collagen, cornea-s			interferon regulat	interferon regulat	hypothetical prote	collagen alpha 1(X	dermal gland prote	serine/t	,	I spli	collagen alpha 1(I		alpha	collagen alpha 1(X		pro	BHLF1 protein - hu
SUMMARIES		S56753	G02474	JC6520	S57837	A35861	A45017	A45064	JC4592	S57836	T50568	152998	A38587	A53340	B31595	A31595	A36330	T31555	A45974	SKXLAG	T36729	T04859	A35363	S59856	T27806	831212	S78476	QQBE8	T29018	OOBE3
	DB	2	~	~	~	~	N	N	~	~	~	~	7	~	7	~	~	~	~	Н	7	~	7	~	~	7	~	П	7	Н
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	% Query Match	28.6	17.7	16.1	13.8	12.2	12.0	11.2	9.5	8.2	6.7	6.4	6.4	6.1	6.1	6.1	6.1	5.9	5.9	ۍ 8	5.8	5.8	5.8	5.7	5.7	5.7	5.7	5.7	5.7	5.6
	Score	780	482.5	440	376	333.5	328.5	306	259.5	224	183	176	176	167	166	166	165.5	160.5	160	159.5	159	158.5	157.5	156.5	156	156	156	156	155	154
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326 PQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEV---- 380 321 QRLVLFPSPASLPDPRQRRYTEDLLE--VAGLRLEQRAGQLLATRLKKCKVFWALSQQLE 378 GGPPGSASPSTPACLLPRNCDTP1FDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSA 440 GGEP-----PLNLIHRDQETTIFDFRVFCTELRDFRDSRRERSPDFTIFLCFGQCFSS 431

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unconventional myo	synapsin I - rat	synapsin Ia - rat	hypothetical prote	mullerian inhibiti	hypothetical prote	collagen alpha 1(I	collagen alpha 1(I	hypothetical prote	collagen alpha 1(X	collagen alpha 1(I	collagen 1 - Caeno		eyelid - fruit fly	collagen alpha 1(X	collagen alpha 2(X
A59266	A25704	A30411	T48814	WFHUM	H70580	CGHULS	CGHU7L	T21314	B40983	CGCH1S	A31219	T00378	T13049	A56101	CGHUZE
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154	150.5	150	149.5	148.5	148	148	148	147	147	146.5	145	145	145	144.5	144.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: 10-oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004
Cispecies: 10-oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004
Cispecies: 10-oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004
Cispecies: 23, 2137-2146, 1995
Nucleic Acids Res. 23, 2137-2146, 1995
Airtle: cIRF-3, a new member of the interferon regulatory factor (IRF) family that is replication: S56753
Airtle: cIRF-3, a new member of the interferon regulatory factor (IRF) family that is replications in S56753
Airtle: circustant in 17 62 AWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKV 121 111 122 YALSRELCWREGPGTDQTEAEAPAAVPPPQ--GGP------PGPFLAHTHAGLQ---- 167 112 YAVA------SGVPNDRGSGGPVAGALQQQPQLLLNHHDLALENTPT 152 269 DGCLPGP----QFQDWRQLEEPLLLGNQPLTGGGCGQDGAGALPVSEECAIPAPSPAEE 262 270 YL----SPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVGHPSCTFLYGPPDPAVRATD 325 263 LLFQSANPAPPPAGDIGGLPPLLDITIYYRGKMVYQEQVDDSRCVLAYQPLDPAV--AE 320 61 62 223 -ACAGGPGLPAGELYGW-AVETTPSPGPQP-----AALTTGEAAAPESPHQAEP 2 ALAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFK 168 -APGPLPAPAGDKGDL-LLQAVQQSCLADHLLTASWGADPVPTKAPGEG--QEGLPLTG-Gaps 92; Length 491; 28.6%; Score 780; DB 2; Length 49: 38.5%; Pred. No. 9.8e-40; tive 60; Mismatches 180; Indels Query Match 28.6 Best Local Similarity 38.5 Matches 208; Conservative 153 208 ò 원 ò 셤 Ś 셤 à g ò 셤 ઠ g 19;

59 26 107 178 176 290 217 342 277

402

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A,Title: An interferon regulatory factor-related gene (xIRF-6) is expressed in the poster A,Reference number: JC6520; MUID:98086218; PMID:9426249
A,Contents: Embryo
A,Accession: JC6520
A,Molecule type: mRNA
A,Residues: 1-459 <-MAT>
A,Content: This protein plays a role in the transcriptional regulation of specific genes C,Goment: This protein plays a role in the transcriptional regulation of specific genes A,Genetics: xIRF-6
C,Superfamily: lymphoid-specific interferon regulatory factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tymphoid-specific interferon regulatory factor - mouse

N;Alternate names: Pip PU.1 interaction partner
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1995 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57837; S57838; I49359
R;Matsuyama, T.; Grossman, A.; Mittruecker, H.W.; Siderovski, D.P.; Kiefer, F.; Kawakami, Nucleic Acids Res. 23, 2127-2136, 1995
A;Title: Molecular cloning of LSIRF, a lymphoid-specific member of the interferon regulating A;Accession: S57836; MUID:95334364; PMID:7541907
A;Accession: S57837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIRROT:064287; EMBL:U20949; NID:g972947; PIDN:AAA75316.1; PID:g97294/
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
A;Note: only a part of the coding sequence is given
B;Matsuyama, T.; Grossman, A.; Mittruecker, H.; Siderovski, D.; Kawakami, T.; Kimura, T., submitted to the EMBL Data Library, June 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 KGDLLLQAVQQSCLADHLLTASWGADPVPTKAP-----GEGQEGLPLTGACAGGPGLPA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 KLFCVETFLSDLISHQKGIITKQPPYEIYLGFGEEWPDGKYKERKLIIVQIIPIVARMII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 FKAWAVARGRWPPSSRGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGD-PADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 HKVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 DDDFEADELNOS------QNHVPISEPFNCLNINDSPIGSSSTGSCT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 VTIMYKGRTVLQKV-VGHP-SCTFLYGPPDPAVRATD-----PQQVAFPSPAELPDQKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 LRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403 PIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHL
                                                                                                                                                                                                                                                                                                                                                                                                                  1 MALAPERAAPRVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFAR-KDLSEADARI
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                                                                                                                                                                                                                                                                                                    463 EGTQREGVSSLDSSDLDLCLSSANSLYDDIECFLMEL 499
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                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 4...
Matches 140; Conservative
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Genetics: Humirfs
A;Gene: Humirfs
C;Superfamily: lymphoid-specific interferon regulatory factor
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JCG520
R;Hatada, S.; Kinoshita, M.; Takahashi, S.; Nishihara, R.; Sakumoto, H.; Fukui, A.; Noda
Gene 203, 183-189, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118
                               500
                                                            TKPKESKLILVKLVPQFCEYWYEQVQRGGASSLNSGNVSLQLSDSFNLFELIEQYHMQTD 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKIY----EVC-SNGP-----APIDSQPPEDYSFGAGEEEEEEELQRMLPSLSLTD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---QVAFPSPABLPDQKQLRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGGPP 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HKVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPG-------PFLAHTH 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                  interferon regulatory factor 5 - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: G02474
R;Grossman, A.; Mittrucker, H.W.; Lantonio, L.; Mak, T.W.
submitted to the EMBL Data Library, March 1996
A;Reference number: H01338
A;Accession: G02474
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                               GRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDLCLSSANSLYDDIECFLMELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HMLPLTD-----DEIKFQYRGRPPRALTISNPHGCRLFYS----QLEATQEQVELFGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FKAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGD-PADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 AGLQAPGPLPAPAGDKGDLLLQAV-----QQSCLADHLLTASWGADPVPTKAPGEGQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPLTGACAGGPGLPAG--ELYGWAVETTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 SACTAVQEPSPGALDVTIMYKGRTVLQKVVGHP-SCTFLYGPPDPAVRATDPQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 482.5; DB 2; Length 504;
; Pred. No. 7e-22;
60; Mismatches 194; Indels 107;
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ilarity 30.0%;
Conservative 6
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Best Local Similarity
Matches 155; Conserv
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                               441
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C;Superfamily: lymphoid-specific interferon regulatory C;Keywords: DNA binding; transcription regulation
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Best Local Similarity 25.7
Matches 120; Conservative
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A;Description: Molecular cloning of LSIRF, a lymphoid-specific member of the interferon A;Reference number: S57838
A;Accession: S57838
A;Accession: S57838
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-450
A;Reference: EMBL: 11692; NID:g790199; PIDN:AAA75309.1; PID:g790200
B;Eisenbeis, C.F.; Singh, H.; Storb, U.
A;Ritle: Pip, a novel IRF family member, is a lymphoid-specific, PU.1-dependent transcrift A;Reference number: 149359; MUID:95317607; PMID:7797077
A;Accession: 149359
A;Status: translated from GB/EMBL/DDBJ
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A;Cross-references: UNIPROT:P23611; GB:M32489; NID:g194088; PIDN:AAA37878.1; PID:g309326
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R;Driggers, P.H.; Ennist, D.L.; Gleason, S.L.; Mak, W.H.; Marks, M.S.; Levi, B.Z.; Proc. Natl. Acad. Sci. U.S.A. 87, 3743-3747, 1990
A;Title: An interferon gamma-regulated protein that binds the interferon-inducible A;Teference number: A35861; MUID:90251633; PMID:2111015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 TTPSPG-PQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 CLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAG----GPGLP----AGELYGWAVE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 MMPPH--DRSW-RDYAPDQSHPEIPYQCPVTFGPRGHHWQGPSCENGCQVTGTFYACAPP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 LQKVVGHP-SCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHL 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interferon consensus sequence-binding protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 QWLIDQIDSGKYPGLVWENEEKSVFRIPWKHAGKQDYNREEDAALFKAWALFKGKF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 ESQAPGIPIEPSIRSAEALA------LSDC------RLHICLYYRDILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS
                                                                                                                                                                                                                                                                                                    A,Residues: 1-450 <RES>
A,Cross-references: EMBL:U34307; NID:g976446; PIDN:AAA75283.1; PID:g976447
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.8%; Score 376; DB 2; Length 450; Best Local Similarity 28.1%; Pred. No. 1.5e-15; Matches 130; Conservative 66; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                 A;Introns: 72/3; 135/1; 164/3; 213/1; 249/1; 367/1; 404/3
C;Superfamily: lymphoid-specific interferon regulatory factor
C;Keywords: alternative splicing
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Best Local Similarity
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A; Status: preliminary
                                                                                                                                                                                                                                                                                 Molecule type: mRNA
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National factor ISGF3 gamma chain - human Nationate names: alpha-interferon-responsive transcription factor cypecies: homo sapiens (man) cypecies: homo sapiens (man) (cypecies: homo sapi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 PGTDQTEAEAPAAVPPPQGGPPGFFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQSCLA 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 QMVISFYYGGKLVGQATTTCLEGCRLSLSQPGLPKLYGPD----GLEP--VCPPTADTI
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                                                                                                                 Indels 159; Gaps
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           Length 424;
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A; Note: part of this sequence was confirmed by protein sequencing C; Superfamily: lymphoid specific interferon regulatory factor C; Keywords: DNA binding; transcription factor
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/ Match 12.2%; Score 333.5; DB 2; Local Similarity 24.3%; Pred. No. 5.1e-13; nes 121; Conservative 65; Mismatches 152;
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gamma (ISGF3 gamma/p48) c
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PDQKQLRYTEEL 349
| ::| :| :|
PSERQRQVTRKL 270
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|: : :
ALFKEK----- 68
                                                RNCDTPIEDFR 408
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RDEVVQVFDTS 324
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-QLYVRQLAEE 379
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                                                                                                CRVHLEGTQRF 468
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Qy 18 LLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVARGRWPPSSRGG 77  146 VLADLPDRTAEAARWETRHFEALRARHTAALDLGQAEHSLPELTALCDGH 195  Qy 78 GPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPAD 117  196 -PLDEPLQALRIRALEDSGRTAEALAAYERVRR-LALADRIGTDFGFELRTLHAELLSPS 252  Qy 118 PHKVYALSRELCWREGPGTDQTEAAPPAVPPPQGGP-PGPFLAHTHAGL 166  10	Qy         227 GPGLPA-GELYGWAVETTPSPGPQPAALTTGEAAAPESPHQAEPYL 271           Db         363 APGTAGPAPGTSYAPGTAPAGTAPABGTAGPARDTSYAPGTTPAPGT 422           Qy         272 SPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVGHPSCTFLYGPPDPAVRAT 324           Db         423 APAFGSTPAPGTAPAPGTAPAPGPQPADGRRPVTGPASGTGPGAAT 468           Qy         325 DPQQVAPSPSPA 335           Db         469 PPEAAAAASAGSAPSPA 485           RESULT 11           15205998	Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cispecies: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004 Ciscesion: 152998 Richa, Y.; Sims, S.H.; Romine, M.F.; Kaufmann, M.; Deisseroth, A.B. DNA Cell Biol. 11, 605-611, 1992 A;Title: Human interferon regulatory factor 1: intron/exon organization. A;Reference number: 152998; MUID:9300481; PMID:1382447 A;Recession: 152998 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Rossiques: 1-325 <res> A;Cross-references: UNIPROT:P10914; GB:L05072; NID:g184648; PIDN:AAA36043.1; PID:gC:Genetics: A;Gene: GDB:IRF1 A;Cross-references: GDB:127269; OMIM:147575 A;Gene: GDB:IRF1 A;Map Position: 5q31.1-5q31.1 A;Introns: 29/3; 63/1; 122/1; 138/3; 182/1; 223/1; 239/3; 285/1</res>	Query Match         6.4%; Score 176; DB 2; Length 325;           Best Local Similarity         23.6%; Pred. No. 0.0011;           Matches         69; Conservative           35; Mismatches         108; Indels           80; Gaps         12;           QY         11 RVLFGEWLLGBISSGCYEGLQWLDEARTCFRVPWKHFARKDLSBADARIFKAWAVARG           B	232A 197 IPVEVVPDST
Db 190TTEATIREPPVFLEHQLPLNSDYSLLLTFIYGRAVVGKTQVHSL 233  Qy 309 SCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTBELLRHVAPGLHLELRGPQLWA 368	RESULT 9 S57836 Lymphoid-specific interferon regulator factor - mouse (fragments) Lymphoid-specific interferon regulator factor - mouse (fragments) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Accession: S57836 R;Matsuyama, T:; Grossman, A.; Mittruecker, H.W.; Siderovski, D.P.; Kiefer, F.; Kawakami Nucleic Acids Res. 23, 2127-2136, 1995 A;Title: Molecular cloning of LSTRF, a lymphoid-specific member of the interferon regula A;Reference number: S57836 A;Reference number: S57836 A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-203 <mat> A;Cross-references EMB: U11692 A;Cross-references EMB: U11692</mat>	03; 36; Gaps 6; AWAVARGRWPPSS 74    :: :: AWALFKGKF 59 VYALSRELCWREG 133   : VYRI 105 6	- Streptomyces coelicolor text_change 09-Jul-2004 sr, A.; Cullum, J.; Kinashi, H.; Hopw netic and physical map for the 8 Mb S 1436	Query Match 6.7%; Score 183; DB 2; Length 1334; Best Local Similarity 28.1%; Pred. No. 0.0018; Matches 106; Conservative 25; Mismatches 150; Indels 96; Gaps 22;

PID:9184649

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R;Harada, H.; Fujita, T.; Miyamoto, M.; Kimura, Y.; Maruyama, M.; Furia, A.; Miyata, T.; Cell 58, 729-739, 1989
A;Fitle: Structurally similar but functionally distinct factors, IRF-1 and IRF-2, bind to A;Reference number: A32828; MUID:89354547; PMID:2475256
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: miNA
A; Residues: 1-68, 'I', 70-96,'R', 98-130,'ER',133-152,'GF',155-163,'A',165-188,'D',190-210,''
& 'T',310-313,' PAPV',318-319,'TP',322-349 ABRN>
A; Cross-references: GB:003168, NID:9198455; PIDN:AAA39333.1; PID:9293676
A; Experimental source: clones 2 and 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interferon regulatory factor 1 - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 29-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: B31595; S04075
R;Miyamoto, M.; Fujita, T.; Kimura, Y.; Maruyama, M.; Harada, H.; Sudo, Y.; Miyata, T.; Jl
A;Tile: Regulated expression of a gene encoding a nuclear factor, IRF-1, that specifical)
A;Reference number: A90903; MUID:88311092; PMID:3409321
                                                                                                                                                                                              A;Accessity type: mRNA
A;Molecule type: mRNA
A;Residues: 1-57, 'R',59-349 <ITO>
A;Cross-references: EMBL:X15949; NID:g33966; PIDN:CAA34073.1; PID:g33967
A;Cross-references: mr. uttommth mr. Kimura, Y.; Maruyama, M.; Furia, A.; Miyata, T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.1%; Score 167; DB 2; Length 349; Best Local Similarity 35.0%; Pred. No. 0.004; Matches 36; Conservative 18; Mismatches 39; Indels
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A;Cross-references: UNIPROT:P14316; GB:L2442
R;Itch, S.; Harada, H.; Fujita, T.; Mimura, T.; Taniguchi,
Nucleic Acids Res. 17, 8372, 1389
A;Title: Sequence of a cDNA coding for human IRF-2.
A;Reference number: S06894; MUID:90045964; PMID:2813069
A;Accession: S06894
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A;COSS-references: UNIPROT:P10914
R;Maruyama, M.; Fujita, T.; Taniguchi, T.
Nucleic Acids Res. 17, 3292, 1989
A;Title: Squence of a cDMA coding for human IRF-1.
A;Reference number: S04075; MUID:89263736; PMID:2726461
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A,Map position: 4035.1-4935.1
C;Reywords: DNA binding; transcription regulation
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A;Molecule type: mRNA
A;Residues: 1-325 MAR.
A;Cross-references: EMBL:X14454
C;Keywords: DNA binding; transcription regulation
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interferror regulatory factor 2 - human
interferror regulatory factor 2 - human
NAlternate names: transcription repressor IRF2
C;Alternate names: transcription repressor IRF2
C;Accession: A53340; 806894; Ā32828
C;Accession: A53340; 806894; Ā32828
R;Cha, Y; Deisseroth, A.B.
J. Biol: Chem, 269, 5279-5287, 1894
A;Title: Human interferon regulatory factor 2 gene. Intron-exon organization and functic A;Accession: A53340; MUID:94148994; PMID:8106512
A;Accession: A53340
A;Accession: A53340
A;Accession: A53340
A;Accession: A53340
A;Accession: A53340
                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-1146 <MBR>
A;Cross-references: UNIPROT:Q90584; EMBL:M60172; NID:g211609; PIDN:AAA48703.1; PID:g2116
A;Accession: A38587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-174,'X',176-233,'X',235-344,'X',346-408,'X',410-499,'X',501-876,'X',878-11
A;Cross-references: GB:M60172
C;Keywords: cornea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 ARGRWPPSSRGG-----GPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPAD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 ARGPPGPSGDTGEPGLTGPQGPPGLPGNPGRPGAK-------GEPGA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHKVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAP-GP--LP- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432 QOGPRGEKGSAVEVVIETIKTEVSSLASQMLSDLQGRAGPPGPPGPPGESVQGLP---GP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 AGGPGLPAGELYGWAVETTPS--PGPQPAALTTGE--AAAPESP------HQAEPYLS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGPPGLPG-----PSGPPGRPGSSVSTSETFVSGPPGPPGPPGPKGDQGE----533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --APAGDKG---DLLLQAV--QQSCLADHLLTASWG--ADPVPTKAPGEGQEGLPLTGAC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----QQV-----AFPSPAELPDQKQLRYTEELL----RHVAPGLHLELRGP 364
                                                                                                 Collagen, cornea-specific - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: S16501, A38587
R;Marchant, J.K.; Linsenmayer, T.F.; Gordon, M.K.
Proc. Natl. Acad. Sci. US.A. 88, 1550-1564, 1991
A;Ftle: cDNA analysis predicts a cornea-specific collagen.
A;Reference number: A38587; MUID:91142213; PMID:1705041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.4%; Score 176; DB 2; Length 1146; Best Local Similarity 23.8%; Pred. No. 0.004; Matches 109; Conservative 31; Mismatches 132; Indels 186;
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R,Miyamoto, M.; Pujita, T.; Kimura, Y.; Maruyama, M.; Harada, H.; Sudo, Y.; Miyata, T.; Cell 54, 803-913, 1988
6-811 54, 803-913, 1988
A;Title: Regulated expression of a gene encoding a nuclear factor, IRF-1, that specifica
A;Reference number: A90903; MUID:88311092; PMID:3409321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: mRNA
A,Residues: 1-329 <MIY>
A,Cross-references: UNIPROT:P15314; GB:M21065; NID:g198458; PIDN:AAA39334.1; PID:g29367;
C,Keywords: DNA binding: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
66 KAGEKEPDPKT-----WKANFRCAMNSLPDIEEVKDQSRNKGSSA--VRVYRMLPPLTKN 118
                                                                            130 -WREGPGTDQTEAEAPAAVPPPQGGPPGPF-----LAHTHAGLQAPGPLPAPAGDKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 RWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRD---NSGDPADPHKVYAL- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 RY----KAGEKEPDPKT-----WKANFRCAMNSLPDIEEVKDQSRNKGSSA--VRVYRML 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 PPLTRNORKERKSKSKBDTKSKTKRKLCGDVSPDTFSDGLSSSTLPDDHSSYTTQGYLGQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 -----DQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQ------APGPLPAPA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 DLDMERDITPALSPCVV-----SSSLSEWHMQMDIIPDSTTDLYNLQVSPMPSTSEA 224
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                                                                                                                                                                                                                                 ---PALSPCAVSSTLPDWHIPVEVV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 RVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARK--DLSEADARIFKAWAVARG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interferon regulatory factor 1 - mouse
C.Species: Mus musculus (house mouse)
C.Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C.Accession: A31595
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                                                                                                                 181 DLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLP-
                                                                                                                                                                                                                                                                                                                      203 PDSTSDLYNFQV----SPMPSISEATTDEDEEGKLPEDIMKLLEQS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.1%; Score 166; DB 2; Length 329; Best Local Similarity 21.6%; Pred. No. 0.0043; Matches 65; Conservative 40; Mismatches 88; Indels 19
                                                                                                                                                                                                                                                                                   232 ---AGELYGWAVETTPSPGPQPAALTTGEAAAPESPHQAEPYLSPS 274
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OM protein - protein search, using sw model

June 18, 2003, 12:42:52; Search time 15 Seconds (without alignments) 1390.840 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-647-965-9
2731
1 MALAPERAAPRVLFGEWLLG......SANSLYDDIECFLMELEQPA 503

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		4 mus m	gallı	homo	homo	P56477 mus musculu	mus	_	hom			Q90871 gallus gall	mus n	рошо	Q02556 homo sapien	mus ก	homo	homo	homo	บรกพ	P23906 mus musculu	rattus	gallus	gallus	_	0	8	Ġ			_	P08121 mus musculu	P09951 rattus norv
SUMMARIES	ΟΊ	IRF7 HUMAN	IRF7 MOUSE	IRF3_CHICK	IRF5 HUMAN	IRF3 HUMAN		IRF3_MOUSE	IRF6_MOUSE	IRF6_HUMAN	IRF4 MOUSE	IRF4 HUMAN	ICSB_CHICK	ICSB_MOUSE	IRTF HUMAN	ICSB_HUMAN	IRTF_MOUSE	IRF1_HUMAN	IRF2_HUMAN	T2D3 HUMAN	IRF1_MOUSE	IRF2_MOUSE	IRF1 RAT	IRF2_CHICK	IRF1_CHICK	XP2_XENLA	SYN1 HUMAN	CA1E_CHICK	TEGU EBV	SYN1_MOUSE	YHL1_EBV			SYN1_RAT
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•	A Query Match	99.4	57.2	28.6	17.9	16.8	16.3	16.0	16.0	15.8	13.8	13.3	12.4	12.2	12.0	11.3	9.5		•	•	•	6.1		•		•	٠	•		•	•	٠	5.6	•
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	P02461 homo sapien P02457 gallus gall						
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                                                                                                                                                                                                                                                                                                                      VYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKG 180
                                                                                                                                                                                                                                                                                                                                                                                            ETTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                               LOKVVGHPSCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRAR 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRAR 420
                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                     DLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAV
                                                                                                                                                                                                                                                  MALAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIF
                                                                                                                                                                                                                                                                  MALAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIF
                                                                                                                                                                                                                                                                                                                                                          DLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAV
                                                                                                                                                                                                                                                                                                                                                                                                                             LQKVVGHPSCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDL
                                                                                                                                                                                                                                Gaps
                                                                                               DNA-binding, Nuclear protein, Activator;
                                                                                                                                         GGPPGPFLAHTHA -> AQGSLLGSCTGGQ (IN
                                                                                                                                                                                                                                ö
                                                                                                        TRXPTOPHAN PENTAD REPEAT.
MALAPE -> MPVPERPAGFDSFRPGTR
D).
                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                Length
                                                                                                                                                                                             AA6A39E0E272727C CRC64;
                                                                                                                                                  ISOFORM C).
MISSING (IN ISOFORM C).
MISSING (IN ISOFORM B).
                                                                                                                                                                                                               Score 2715; DB 1;
Pred. No. 3.8e-148;
                                                                                                                                                                            E -> K (IN REF. 2)
Q -> R (IN REF. 3)
                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLSSANSLYDDIECFLMELEOPA 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLSSANSLYDDIECFLMELEOPA 503
                                                 Pfam; PF00605; IRF; 1.
PRINTS; PR00267; INTERNREGFCT.
Probom; PD002355; IRF; 1.
PROSITE; PR00348; IRF; 1.
Transcription regulation; DNA-b:
                                                                                                                                                                                              54278 MW;
                                                                                                                                                                                                               99.4%;
AF076494; AAC70999.1;
                                          InterPro; IPR001346; IRF.
                                                                                                                                                                                                                       Local Similarity 99.4
nes 500; Conservative
              TRANSFAC; T04674; -. Genew; HGNC:6122; IRF7.
                                                                                                                                                                   256
                                                                                                                                          164
                                                                                                        Alternative splicing
                                                                                                                                                                                             503 AA;
                                                                                                                                          152
                                  MIM; 605047;
                                                                                                               DNA BIND
VARSPLIC
                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                              SEQUENCE
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IRF7 MOUSE
ID IRF7 MC
AC P70434,
DT 01-NOV-
DT 16-OCT-
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interferon regulatory factor 7 (IRF-7).

Ā

457

STANDARD;

MOUSE

P70434;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELY-GW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 LELRGPSLWALRMGKCKVYWEVGSPMGTTGPSTPPQLLERNRHTPIFDFSTFFRELEEFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 AVETTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 QVEAVPSPRPQQPALT-------ERSLGFLDVTIMYKGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFR
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                                                                                                                                                                                                                                                                                                                                              o
                                                                                                                                                                             STRAIN-BALB/C; TISSUE-Spleen;
Grossman A., Nicholl J., Antonio L., Luethy R., Suggs S.,
Sutherland G.R., Mak T.W.;
Sutherland G.R., Mak T.W.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INTERFERON-
STIMULATED RESPONSE ELEMENT (ISRE) IN IFN PROMOTERS AND IN THE
PROMOTER (QP) OF EBV NUCLEAR ANTIGEN-1 (EBNA1) (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; DNA-binding; Nuclear protein; Activator.
DNA BIND 11 122 TRYPTOPHAN PENTAD REPEAT.
SEQUENCE 457 AA; 51222 MW; 30B102C668F56142 CRC64;
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 57.2%; Score 1562; DB 1; Length 4
Best Local Similarity 62.6%; Pred. No. 1.7e-82;
Matches 315; Conservative 36; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00267; INTFRNREGFCT.
ProDom; PD002355; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U73037; AAB18626.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1859212; Irf7.
InterPro; IPR001346; IRF.
Pfam; PF00605; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00348; IRF; 1.
PROSITE; PS00601; IRF; 1.
Mus musculus (Mouse)
                                                                                                                                                      FROM N.A.
                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359
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                                                  208 DGCLPGP-----QFQDWRQLEEPLLLGNQPLTGGGCGQDGAGALPVSEECAIPAPSPAEE 262
                                                                                                                                                                                                                                                        270 YL----SPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVGHPSCTFLYGPPDPAVRATD 325
                                                                                                                                                                 263 LLFQSANPAPPPPAGDIGGLPPLLDITIYYRGKWYYQEQVDDSRCVLAYQPLDPAV--AE 320
                                                                                                                                                                                                                          326 POQVAFPSPAELPDOKOLRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEV---- 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 GRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDLCLSSANSLYDDIECFLMELE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding; Nuclear protein.
TRYPTOPHAN PENTAD REPEAT.
POLY-GLU,
EDVKWPPTLQPPTLR -> DAVQSGPHMTPYSLLKEDVKW
------AALTTGEAAAPESPHQAEP
                                                                                                                                                                                                                                                                                                                                                                          381 GGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. SUBMITLAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grossman A., Mittrucker H.W., Lantonio L., Mak T.W.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IN REF. 1).
01B2ED95C28384E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      013568; 0980P0;
01-NOV-1997 (Rel. 35, Created)
15-UUN-2002 (Rel. 41, Last sequence update)
Interferon regulatory factor 5 (IRF-5).
  223 -ACAGGPGLPAGELYGW-AVETTPSPGPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC004201; AAH04201.1; -. EMBL; BC004139; AAH04139.1; -. HSSP; P23906; IIRF. Genew; HGNC:6120; IRFS. InterPro; IPR001346; IRF.
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PRINTS, PR00267; INTFRNREGFCT.
ProDom; PD002355; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56044 MW;
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PROSITE; PS00601; IRF; 1.
Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U51127; AAA96056.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118
149
175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. TISSUE=Kidney;
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161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 YALSRELCWREGPGTDQTEAEAPAAVPPPQ--GGP-----PGPFLAHTHAGLQ---- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 YAVA-----SGVPNDRGSGGPVAGALQQQPQLLLNHHDLALENTPT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 -APGPLPAPAGDKGDL-LLQAVQQSCLADHLLTASWGADPVPTKAPGEG--QEGLPLTG- 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ALAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFK
                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Interferon regulatory factor 3 (IRF-3).
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0267; INTFRNREGFCT.
Prodom; PD002355, IRF; 1.
SWART; SM00348; IRF; 1.
PROSITE; PS00601; IRF; 1.
Transcription regulation; DNA-binding; Nuclear protein; Activator.
DNA BIND 14 112 TRYPTOPHAN PENTAD REPEAT.
SEQÜENCE 491 AA; 54441 MW; CAE0C2AA8BE976D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92;
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                                                                                                                                                                                                     491 AA.
                                433 GLCLSSTNSLYEDIEHFLMDLGQ 455
     DLCLSSANSLYDDIECFLMELEQ 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U20338; AAA86995.1; -. HSSP; P15314; 1IF1.
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Matches 208; Conservative
                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                     CHICK
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Best Local S
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Q90643;
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                                                                                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                 YKIY----EVCSNGPAPTDSQPPEDYSFGAGEEEEEEELQRMLPSLSLTEDVKWPPTLQ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427
                                                                                                                                                                                                                                              FKAWAKETGKYTEG------VDEADPAKWKANLRCALNKSRDFRLIYDGPRDMPPQP 114
                                                                                                                                                                                                                                                                                                                                                                                        PPQGGPPGPFLAHTHAGLQAP-----GPLPAPAGDKGDLLLQAVQQSCLADHLLTAS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WGADPVPTKAPGEGOEGLPLTGACAGGPGLPAG--ELYGWAVETTPSPGPQPAALTTGEA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --QLEATQEQVELFGPISLEQVRFPSPEDIPSDKQRFYTNQLLDVLDRGLILQLQGQDLY 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIRLCOCKVFW--SGPCASAHDSCPN-PIQREVKTKLFSLEHFLNELILFOKGOTNTPPP 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PGNPAGFRELLSEVLE----PGPLPASL---- 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --PPAGEQLLPDLLISPHMLPLTD----LEIKFQYRGRPPRALTISNPHGCRLFYS-- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPAVRATDPQ-----QVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQLW 367
                                                                                                                                               63
                                                                                                                                                                                                 FKAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGD-PADP
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MEDLINE-99020108; PubMed=9803267;

MEDLINE-99020108; PubMed=9803267;

Bellingham J., Gregory-Evans K., Gregory-Evans C.Y.;

Mapping of human interferon regulatory factor 3 (IRF3) to chromosome 19q13.3-13.4 by an intragenic polymorphic marker.";

Ann. Hum. Genet. 62:231-234(1998).

-I-FUNCTION: MAY ACTIVATE TRANSCRIPTION BY COMPLEX FORMATION WITH OTHER TRANSCRIPTIONAL FACTORS, POSSIBLY MEMBERS OF THE STATFANKSCRIPTIONAL FACTORS, POSSIBLY MEMBERS OF THE STATFANKING. BALLY. BINDS SPECIFICALLY TO THE IFN-STIMULATED RESPONSE ELEMENT
                                                                                                                             -----PAAVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVGHP-SCTFLYGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRGSPR
                                                                                                 1 MALAPERAAPRVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLS-EADARI
                                                       Gaps
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"Identification of a member of the interferon regulatory factor
family that binds to the interferon estimulated response element and
activates expression of interferon-induced genes.";
Proc. Natl. Acad. Sci. U.S.A. 92:11657-11661(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
17.9%; Score 487.5; DB 1; Length 498; 28.9%; Pred. No. 3.1e-21; ive 59; Mismatches 173; Indels 147;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
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TISSUE-Retina;
MEDLINE-96102173; PubMed=8524823;
                                               Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                           Similarity
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     Query Match
Best Local
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IRF3 HUMAN
ID 146534
AC Q146534
DT 01-NOV
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DB INTERF6
GN IRF3
OC MAMMAIN
OX NCBI T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 PAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEP-SPGALDVTIMYKGRTVLQKVVGHP 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 ARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDL 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 SCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 WPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSRELC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 WREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLRSPSLDNPTP-----FPNLGPSENPLKRLLVPGEEWEFEVTAFYRGRQVFQQTISCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 SCTFLYGPPDPAVRATDPQQVAFPSPA-ELPDQKQLRYTEELLRHVAPGLHLELRGPQLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-binding; Nuclear protein; Activator;
                                                     Q
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llarity 28.0%; Pred. No. 1.3e-19;
Conservative 64; Mismatches 191; Indels 108;
(ISRE) BUT NOT TO THE IRF-1 BINDING SITE PRD-I.
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: EXPRESSED CONSTITUTIVELY IN A VARIETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRYPTOPHAN PENTAD REPEAT.

R -> Q (IN DESNP:968457).

FTIG-VAR 011901.

E -> K (IN DBSNP:1049486).

/FTIG-VAR 011902.

S -> T (IN DBSNP:7251).

/FTIG=VAR_011903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTId=VAR 011903.
F536676FA78B0110 CRC64;
                                                                                                         SIMILARITY: BELONGS TO THE IRF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 -NSGVG----DFSQPDTSPDTNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47219 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00267; INTFRNREGFCT
                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z56281; CAA91227.1; -. EMBL; U86636; AAC68818.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001346; IRF. Pfam; PF00605; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew, HGNC:6118; IRF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107
96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00348; IRF;
PROSITE; PS00601; IRI
                                                                                                                                                                                                                                                                                                                                                                                                                          P23906; 2IRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                               FRANSFAC; T04673; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     427 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 141; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD002355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 603734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEOUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
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Matches
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248 ---DLEIKFQYRGKAPRTLTISNPQGCRLFYS----QLEATQEQVELFGPVTLEQVRFPS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 ARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALS
285 SPGALDVIIMYKGRIVLQKVVGHP-SCTFLYGPPDPAVRAIDPQ-
                                                                                                                                                                454 EPWLCRVHLEGTQREGVSSLDSSDLDL 480
                                                                                                                                                                                          418 VPVAARLLLEMFSGELSWSADSIRLOI 444
                                                                                                                                                                                                                                                                                                                                Interferon regulatory factor 3 (IRF-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00267; INTERNREGFCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U75839; AAB36924.1; -. EMBL; U75840; AAB36925.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001346; IRF. Pfam; PF00605; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 27.6
Matches 143, Conservative
                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00348; IRF; 1.
PROSITE; PS00601; IRF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1859179; Irf3.
                                                                                                                                                                                                                                                                                                                                                            musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P23906; 2IRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D002355;
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                       01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                             IRF3 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom;
                                                                                                                                                                                                                                                                             8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 WPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGD-PADPHKVYALSREL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 CWREGP------GIDQIEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 AGDKGDLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGEL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----XSLPKEDTKWPPALQPPVGL-----GPPVPDPNL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 YGWAVETTPSPGPQ-----PAALTTGEAAAPESPHQAEPYL----SPSPSACTAVQEP 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 RVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 RVRLKPWLVAQVNSCQYPGLQWVNGEKKLFYIPWRHATRHGPSQDGDNTIFKAWAKETGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                          Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.3%; Score 444.5; DB 1; Length 497; 29.2%; Pred. No. 8.7e-19; ive 58; Mismatches 188; Indels 113
                                                                                                                                                                                                                                                                         STRAIN=CS7BL/6J; TISSUB=Lymph node; Grossman A., Kondo S., Antonio L., Mak T.W.; Submitred (NOV-1997) to the EMBL/GenBank/DDBJ databases.-:- SUBCELL/LAR LOCATION: Nuclear.-:- SUBCELL/LAR LOCATION: Nuclear.-:- SIMILARITY: BELONGS TO THE IRF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWART; SMUU-40; 11...;
PROSITE; PS00601; IRF; 1.
Transcription regulation; DNA-binding; Nuclear protein.
DNA_BIND 16 118
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-GLU.
D8BD54DB946E354F CRC64;
                                                                                                                                     15-JUL-1998 (Rel. 36, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Interferon regulatory factor 5 (IRF-5).
                                                                                              497 AA
  DLCLSSANSL --- YDDIECFLMEL 499
                            415
                  || :|:: | | : | | DLHISNSHPLSLTSDQYKAYLQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1350924; Irf5.
InterPro; IPR001346; IRF.
Pfam; PR00605; IRF; I.
PRINTS; PR00267; INTERNEGFCT.
ProDom; PD002355; IRF; I.
SMART; SM00348; IRF; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 148 P(
497 AA; 56005 MW;
                                                                                                                         (Rel. 36, Created)
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF028725; AAB81997.1;
HSSP; P23906; 1IRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 148; Conservative
                                                                                                STANDARD;
                                                                                                                                                                                              musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                         15-JUL-1998
                                                                                             IRF5 MOUSE
P56477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
 479
                            392
                                                                                                                                                                                                                                                                 SEQUENCE
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Best Local &
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                                                                                                                                                453
                                                                                                                                                                                                                         417
PAEL POOKQLRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAINE-BALB(C; TISSUE-Liver;
Hakem R., Grossman A., Antonio L., Suggs S., Mak T.W.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY ACTIVATE TRANSCRIPTION BY COMPLEX FORMATION WITH
COTHER TRANSCRIPTIONAL FACTORS, POSSIBLY MEMBERS OF THE STAT
FAMILY. BINDS SPECIFICALLY TO THE IRN-STIMULATED RESPONSE ELEMENT
(ISRE) BUT NOT TO THE IRP-1 BINDING SITE PRD-1 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE IRP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 ERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFKAWAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 CLLPRNCDTPIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKL
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; DNA-binding; Nuclear protein; Activator.
DNA BIND 7 107 TRYPTOPHAN PENTAD REPEAT.
SEQUENCE 419 AA; 46852 MW; 1FF67C4E0FC7F027 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota. Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.0%; Score 438; DB 1; Length 419; 27.6%; Pred. No. 1.7e-18; tive 56; Mismatches 182; Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419 AA
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| | : | | | | | | | | | ASGAYTP----GKDKPDVST----WKRNFRSALNRKEVULRLAAADNSKDPYDPHKVYEFV 110
                                                                                                                                 238
                                                                                           T-----PGARDFVHLGASPDTNGKSSLPHSQENLPKLF-----DGLILGPLKD 153
                                                                                                                                                                                                                                                                              TIMYKGRIVLOKVVGHPSCTFLYGPPDPAVRATDPQQVAFPSP-AELPDQKQLRYTEELL 350
                                                                                                                                                                                                                                                                                                                                                      401
                                                                                                                                                                                                                                                                                                                                                                                      KGLGNGLALWQAGOCLWAQRLGHSHAFWALGEELLPDSGRGPDGE------VHKDKD 309
                                                                                                                                                                                                                                                                                                                                                                                                                             TPIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVH 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 GAVFÖLRPFVADLIAFMEGSGH-SPRYTLWFCMGEMWPQDQPWVKRLVMVKVVPTCLKEL 368
                                                       RELCWREGPGT-----DQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGD
                                                                                                                             179 KGDLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGW
                                                                                                                                                                                                                                          -----ENPLKOLLAEEQWEFEV
                                                                                                                                                                                                                                                                                                                TAFYRGRQVFQQTLFCPGGLRLVG -- STADMTLPWQPVTLPDPEGFLTDKLVKEYVGQVL
                                                                                                                                                                                                                                                                                                                                                    RHVAPGLHLELRGPQLWARRMGKCKVYWEVG------GPPGSASPSTPACLLPRNCD
                                                                                                                                                                                                     239 AVETTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGAL----DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BALB/C; TISSUE=Colon; Grossman A., Mittrucker H.W., Antonio L., Mak T.W.; Grossman A., Mittrucker H.W., Antonio L., Mak T.W.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.-!- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcription regulation; DNA-binding; Nuclear protein.
DNA BIND 9 111 TRYPTOPHAN PENTAD REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53106 MW; 68CCAA90680FEDC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | : | | | : | | | LEMAREGGASSLKTVDLHISNSQPISLTSDQYKAYLQDL 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEGIQREGVSSLDSSDLDLCLSSANSL-YDDIECFLMEL 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Interferon regulatory factor 6 (IRF-6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467
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InterPro; IPRO01346; IRF.
Pfam; PF00605; IRF; 1.
PRINTS; PR00267; INTER; 1.
ProDom; PD002355; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U73029; AAB36714.1; -.
HSSP; P23906; 2IRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00348; IRF; 1. PROSITE; PS00601; IRF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  467 AA;
                                                                                                                                                                 EGSSDLAIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          -SOOLPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRF6 MOUSE
                                                                                                                                                                                                                                                                                                                201
                                                       126
                                                                                                                                                                   154
                                                                                                                                                                                                                                                                              292
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                                                                                                                                                                                                                                                                                                                                                                                      259
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                                                                                                                                                                                                                                          991
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                     348 LETFLSBLIAHQKGQIEKQPPFEIXLCFGEEWPDGKPLERKLILVQVIPVVARMIYEMFS 407
                                                                                                                                                                                                                                                                                                    136 EKDNDVDEDEE----EDELEQSQHHVPIQDTFPFLNINGSPMAPASVGNCSVGNCSP--- 188
                                                                                                                                                                                                                                                                                                                                      LYGWAVETTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIM 294
                                                                                                                                                                                                                                                                                                                                                                      -----ESVWPKTEPLEMEVPQAPIQPFYSSPELWISSLPMT-----DLDINKFQ 231
                                                                                                                                                                                                                                                                                                                                                                                                         295 YKGRTVLQKV-VGHP-SCTFLYGPPDP-----AVRATDPQQVAFPSPAELPDQKQLRYT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 EELLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFD 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         407 FRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQ 466
                                                                                                   99
                                                                                                                                                                                                                         1 MALAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFAR-KDLSEADARI
                                                                                                                                    FKAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGD-PADP
                                                                                                                                                                                                    HKVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGD
                                                                                                                                                                                                                                                                    179 KGDLLLOAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPL----TGACAGGPGLPAGE
                                                                                                 1 MALHPR----RVRLKPWLVAQVDSGLYPGLIWLHRDSKRFQIPWKHATRHSPQQEEENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
Homo.
                                 88;
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Length 467;
                                 211; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.-!- SUBCELLULAR LOCATION: Nuclear (Potential).-!- SIMILARITY: BELONGS TO THE IRF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grossman A., Mittrucker H.W., Antonio L., Ozato K., Mak Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; E
Catarrhini; Hominidae;
Query Match
Best Local Similarity 27.7%; Pred. No. 2.5e-18;
Matches 142; Conservative 72; Mismatches 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | | | : | : | : | : | : | 408 GDFTRSFDSGSVRLQISTPD-IKDNIVAQLKQL 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467 REGVSSLDSSDLDLCLSSANSLYDDIECFLMEL 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Interferon regulatory factor 6 (IRF-6).
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Mammalia; Eutheria; Primates;
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Submitted (JUN-1998)
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Mak T.W.;
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
    the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                       60 FKAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGD-PADP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                   57 FKAWAVETGKY---QEGVDDPDPAK-----WKAQLRCALNKSREFNLMYDGTKEVPMNP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 HKVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 VKIY----QVC------DIPQPQG------SIINPGSTGSAPWD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 KGDLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPL----TGACAGGPGLPAGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 LYGWAVETTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIM 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 ---w-----pkteplemevpQ--apiQpfysspelwisslpmr-----DldikfQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 YKGRTVLQKV-VGHP-SCTFLYGPPDP-----AVRATDPQQVAFPSPAELPDQKQLRYT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 YRGKEYGÓTMTVSNÞQGCRLFYGDLGÞMPDQEELFGPVSLEQVKFÞGPEHITNEKQKLFT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 EELLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFD 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 SKLLDVMDRGLILEVSGHAIYAIRLCQCKVYWSGPCAPSLVAPN----LIEROKKVKLFC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            407 FRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQ 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 EKD---NDVDEEDEEDE-LDQSQHHVPIQDTFPFLNINGSPMAPASVGNCSVGNCSPEAV 191
                                                                                                                                                                                                                                                                                                                                                  59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _IRF4_MOUSE STANDARD, PRT, 450 AA.

Q64287; Q60802;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Interferon regulatory factor 4 (IRF-4) (Lymphocyte specific interferon regulatory factor 1 (IRF-4) (Lymphocyte specific interferon (Transcriptional activator PIP).
                                                                                                                                                                                                                                                                                                                                                                     1 MALAPERAAPRVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFAR-KDLSEADARI
                                                                                                                                                                                                                                                                                                                        88;
                                                                                                                                                                                                                                                                                          15.8%; Score 431; DB 1; Length 467; 27.7%; Pred. No. 4.8e-18; Live 72; Mismatches 211; Indels
                                                                                                                                                                                                                                    Transcription regulation; DNA-binding; Nuclear protein.
DNA BIND 9 111 TRYPTOPHAN PENTAD REPEAT.
SEQUENCE 467 AA; 53129 MW; 7E28F5E0F5E0F5EA4053 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467 REGVSSLDSSDLDLCLSSANSLYDDIECFLMEL 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AF027292; AAB84111.1; -. EMBL, AL022398; CAA18545.1; -. EMBL, BC014852; AAH14852.1; -. HSSP; P23906; 21RP.
                                                                                                                                                                                PRINTS; PR00267; INTFRNREGFCT. ProDom; PD002355; IRF; 1.
                                                                                                                                                     InterPro; IPR001346; IRF. Pfam; PF00605; IRF; 1.
                                                                                                                                                                                                                        PROSITE; PS00601; IRF; 1.
                                                                                                                                                                                                                                                                                                          Local Similarity 27.7
hes 142; Conservative
                                                                                                                                         Genew, HGNC:6121; IRF6
                                                                                                                                                                                                           SMART; SM00348; IRF;
                                                                                                                                                                                                                                                                                             Query Match
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IRR4 MOUSE
ID RA4 MOUSE
OR4287,
DT 01-NOV-
DT 15-JUN-
DE INTERFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
PRODUCED BY ALTERNATIVE SPLICING; THEY ONLY DIFFER IN THE PRESENCE
OR ABSENCE OF A GLUTAMIC ACID RESIDUE.
-!- TISSUE SPECIFICITY: LYMPHOLID CELLS.
-!- INDUCTION: NOT INDUCED BY INTERFERONS.
-!- SIMILARITY: BELONGS TO THE IRF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C55BL/6, and 129/SvJ; TISSUE-Spleen;
MEDLINE-95334364; PubMed-7541907;
Matsuyama T., Grossman A., Mitrruecker H.-W., Siderovski D.P.,
Kiefer F., Kawakami T., Richardson C.D., Taniguchi T., Yoshinaga S.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 REGIDKEDPPT-----WKTRLRCALNKSNDFEELVERSQLDISDPYKVYRI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning of LSIRE, a lymphoid-specific member of the interferon regulatory factor family that binds the interferon-stimulated response element (ISRE).";

Nucleic Acids Res. 23:2127-2136 (1995).

-!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INTERFERON-STIMULATED RESPONSE ELEMENT (ISRE) OF THE MHC CLASS I PROMOTER. BINDS THE IMMUNOSIOBLIAN LAMBDA LIGHT CHAIN ENHANCER, TOGETHER WITH PULL. PROBABLY PLAYS A ROLE IN ISRE-TARGETED SIGNAL TRANSUCTION MECHANISMS SPECIFIC TO LYMPHOID CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation; DNA-binding; Nuclear protein; Activator; Alternative splicing.
                         Craniata, Vertebrata, Euteleostomi;
Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.8%; Score 376; DB 1; Length 450; 28.1%; Pred. No. 6.3e-15;
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                                                                                                                                                                                                             MEDLINE=95317607; PubMed=7797077;
Eisense C.F., Singh H., Storb U.;
"Pip, a novel IRF family member, is a lymphoid-specific,
PU.1-dependent transcriptional activator.";
Genes Dev. 9:1377-1387(1995).
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR00267; INTFRNREGFCT
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EMBL, U11692, AAA75309.1; --
EMBL, U20949; AAA75316.1; --
EMBL, U20949; AAA75317.1; --
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Matches 130; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                               NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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-!- INDUCTION: NOT INDUCED BY INTERFERONS
-!- SIMILARITY: BELONGS TO THE IRF FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431 PEHISNPEDYHRSI 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00348; IRF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFAC; T04929;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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      SOUTH THE TENT OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        KELTTTSPEGCRISHG---HTYDVSNLDQVLFPYP---DDNGQRKNIEKLLSHLERGLVL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417
                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                    TTPSPG-PQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTV 300
                                                                                                                                                                                                                                                                                                                                                                                                                    LQKVVGHP-SCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGTDQTEAEAPAAVPPPQGGPPGP---FLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTRA TOUGHN SIANDARD; FRI; 451 AA.
(15306; 09660; 18. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UNOV-2002 (Rel. 41, Last annotation update)
Interferon regulatory factor 4 (IRF-4) (Lymphocyte specific interferon regulatory factor) (LSIRF) (NF-EMS) (Multiple myeloma oncogene 1).
IRF4 OR MUM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING: THEY ONLY DIFFER IN THE PRESENCE OR ABSENCE OF A GLUTAMIC ACID RESIDUE.
TISSUE SPECIFICITY: LYMPHOID CELLS.
                                                                                                                                                                                                        ----VPEGAKKGAKOLTLDDTQMAMGHPYPMTAP---YGSLPAQQVHNY
                                                                                                                                                             CLADHLLTASWGADPVPTKAPGEGOEGLPLTGACAG----GPGLP----AGELYGWAVE
                                                                                                                                                                                                                                                                                                                                                      -----LSDC-----RLHICLYYRDILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELRGPQLWARRMGKCKVYWEVGGPPGSAS - - PSTPACLLPRNCDTPIFDFRVFFQELVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosomal
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INTERFERON-
BINDS THE INMUNOGLOBULIN LANABA LIGHT CHAIN ENHANCER, TOGETHER
WITH PU.1. PROBABLY PLAYS A ROLE IN ISRE-TARGETED SIGNAL
TRANSDUCTION MECHANISMS SPECIFIC TO LYMPHOID CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grossman A., Mittrucker H.W., Nicholl J., Suzuki A., Chung S., Antonio L., Sugga S., Sutherland G.R., Siderovski D.P., Mak T.W.; Cloning of human lymphocyte-specific interferon regulatory factor (h.GIRF/hIRF4) and mapping of the gene to 6p23-p25."; Genomics 37:229-233(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryora, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lida S., _buller M., Hatzivassiliou G., Pulivarthi R., Klein B.,
Corradini P., Boccadoro M., Nilsson K., Chaganti R.S.K.,
Dalla-Favera R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Deregulated expression of MUM1 gene by t(6,14) (p25,q32)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translocation in multiple myeloma.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCR 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451
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                                                                                                                                                                                                                                                                                                                                                      ESOAPGIPIEPSIRSAEALA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97079690; PubMed=8921401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 QKVVGHP-SCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 -GAKQLTLEDPQM-----SMSHPYT-MTTPYPSLPA------QQVHNYMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 EWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 QWLIDQIDSGKYPQLVWENEEKSIFRIPWKHAGKQDYNREEDAALFKAWALFKGKF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGP-LPAPAGDKGDLLLQAVQQSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 ADHILITASWGADPVPIKAPGEGQEGLPLT------GACAGGPGLPAGELYGWAVET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 PP--LDRSW-RDYVPDOPHPEIPYOCPMTFGPRGHHWOGPACENGCQV-TGTFYACAPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 TPSPG-PQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 LRGPQLWARRMGKCKVYWEVGGPPGSAS--PSTPACLLPRNCDTPIFDFRVFFQELVEFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 MAPDGLYAKRLCQSRIYWD--GPLALCNDRPNK----LERDQTCKLFDTQQFLSELQAF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 ARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AHHGRSLPRFQVTLCFGEBFPDPQ-RQRKLITAHVEPLLARQLYYFAQQNSGHFLRGYDL
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Transcription regulation; DNA-binding; Nuclear protein; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92;
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306 K -> N (IN REF. 2).
333 R -> T (IN REF. 2).
51772 MW; 17CD1327C6F5BFFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRYPTOPHAN PENTAD REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISSING (IN ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.5%; Pred. No. 3.5e-14; ive 73; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.3%; Score 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR00267; INTFRNREGFCT. PD002355; IRF; 1.
                                                                                                                                                                                                                                 EMBL; U52682; AAC50779.1; -. EMBL; U63738; AAB37258.1; -.
                                                                                                                                                                                                                                                                                         BC015752; AAH15752.1;
P23906; 2IRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 DLCLSSANSLYDDI 492
                                                                                                                                                                                                                                                                                                                                                                                               MIM, 601900, -.
InterPro; IPR001346; IRF.
Pfam; PF00605; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:6119; IRF4.
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165
300
306
333
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EMBL; M32489; AAA37878.1; -.
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InterPro; IPR001346; IRF.
                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00605; IRF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P23906; 2IRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRANSFAC; T00402; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
186 PS----
                                                                                                                                                                                                                                                                                     ICSB MOUSE
P23611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQÜENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 AVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 EGPG-----TDQTEAE-APAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----CVDEYL-----GIIKRSPSPOG-----TCRNPP-----IPDWWMQ-QPS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 PGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPG--ALDVTIMYKGRTVLQK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 RGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYAL--SRELCWR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 -----KEGDKAEPATWKTRLRCALNKSPDFEEVTDRSQLDISEPYKVYRIVPEEBQKCK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                    "Chicken interferon consensus sequence-binding protein (ICSBP) and interferon regulatory factor (IRF) 1 genes reveal evolutionary conservation in the IRF gene family."

Proc. Natl. Acad. Sci. U.S.A. 97:3105-3109 (1995).

-!- FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION OF TYPE I IFM AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON CONSENSUS SEQUENCE (ICS)). PLAYS A REGULATORY ROLE IN CELLS OF THE IMMUNE SYSTEM (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 EWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS
                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
11cterferon consensus sequence binding protein (ICSBP).
1CSBP1 OR ICSBP.
6allus gallus (Chicken).
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.4%; Score 338; DB 1; Length 425;
24.3%; Pred. No. 8.7e-13;
ive 77; Mismatches 168; Indels 132; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; DNA-binding; Activator; Nuclear protein.
DNA BIND 9 110 TRYPTOPHAN PENTAD REPEAT.
SEQÜENCE 425 AA; 49171 MW; 92BB8A9B77024EB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                 MEDLINE=95241453; PubMed=7536924;
Jungwirth C., Rebbert M., Ozato K., Degen H.J., Schultz U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 IGVGNGSSLTDVGDMDCSPSAIDDLMKEPP-------
                                         425 AA.
                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE IRF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00267; INTFRNREGFCT.
ProDom; PD002355; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L39767; AAA62159.1; -.
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                                         STANDARD;
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                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P23906;
                                       CHICK
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                                                                                                                                                                                                                                        413
                                                                                  304 VVGHPSCTFLYG-----PPDPAVRATDP---QQVAFPSPAELPDQKQLRYTEELLRHV 353
                                                                                                                                                         276
                                                                                                                                                                                                                                                                                         414 LVEFRARORRGSPRYTIYLGFGODLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSL 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 LOQYYNNQGR-PPDSRVMLCFGEEFPDTVPLRCKLILVQVEQLCVRQVMEEAGKTCSSPM 391
                                                                                                                            354 APGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQE
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-i. FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION
-OF TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON
CONSENSUS SEQUENCE (ICS)). PLAYS A REGULATORY ROLE IN CELLS OF THI
IMMUNE SYSTEM.
--LPLVNGYTGYEQHHSGYSQMVITFFYSGR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Driggers P.H., Ennist D.L., Gleason S.L., Mak W.-H., Marks M.S.,
Levi B.-Z., Flanagan J.R., Appella E., Ozato K.;
"An interferon gamma-regulated protein that binds the interferon-
inducible enhancer element of major histocompatibility complex class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00348; IRF; 1.
PROSITE; PS00601; IRF; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein; Interferon induction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: Nuclear.
-i- TISSUE SPECIFICITY: PREDOMINATLY IN LYMPHOID TISSUES.
-i- INDUCTION: BY INTERFERON GAMMA.
-i- SIMILARITY: BELONGS TO THE IRF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 110 TRYPTOPHAN PENTAD REPEAT.
424 AA; 48237 MW; FBE79A76846E8EB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Interferon consensus sequence binding protein (ICSBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474 DSSDL------DLC 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 LPDDVQQEQVYRIFQDIC 409
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ProDom; PD002355; IRF; 1.
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112
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                                                                                                                                                                                                                                A45017; A45017.
                                                                                                                                                                                                                                                                                                                                                                                                                393 AA;
                                                                                                                                                                                                                                            HSSP; P23906; 2IRF
                                                                                                                                                                                                                                                                              MIM; 147574;
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Matches
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                                   19;
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                                                                                                                                                                                                                                                      253 LTTGEAAAPESPHQAEPYLSPSPSACTA-----VQEPSPG------ALD----- 290
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                                                                                                                                                                                                                                                                                                      337
                                                                                                                                                                                                                                                                                                                   :: | |: | |: | |: | OWVISFYYGGKLVGQATTTCLEGCRLSLSQPGLPKLYGPD----GLEP--VCFPTADTI 256
                                                                                                          133
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                                                                                                                                                                                                                                                                                                                                                    PDQKQLRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLP 397
                                                                                                                                                                                                                                                                                                                                                                                                   RNCDTPIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWL 457
                                                                                                                                                                               ------CMS 131
                                                                                                                                                                                                                                                                                                                                                                                                                  74
                                                                                67
                                                                       RGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREG
                                                                                                                       -----KEGDKAEPATWKTRLRCALNKSPDFEEVTDRSQLDISEPYKVYRI
                                                                                                                                                        PGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQSCLA
                                                                                                                                                                                                       DHLLITASWGADPVPTKAPGEGQ - EGLPLIGACAGGPGLPAGELYGWAVETTPSPGPQPAA
                                                                                                                                                                                                                              E-----VPEMECGRSEIBELIKE------PSVDEYMGMTKRSPSP----
                                                                                                                                                                                                                                                                              ------PEACRSQILPDWWVQQPSAGLPLVTGYAAYDTHHSAFS
                                                                                                                                                                                                                                                                                                      ---VIIMYKGRIVLOKV------VGHPSCIFLYGPPDPAVRATDPQQVAFPSPAEL
                                                         EWILGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding proteins.;
Mol. Cell. Biol. 12:3315-3324 (1992).
-!- FUNCTION: RESPONSIBLE FOR THE INITIAL STIMULATION OF INF-ALPHA-RESPONSIVE GENES. IT RECCGNIZES AND BINDS TO THE INF-STIMULATED RESPONSIVE ELEMENT, OR ISRE WITHIN THE REGULATORY SEQUENCES OF TRAGET GENES. ISGF3 PLAYS A PRIMARY ROLE IN THE TRANSMISSION OF SIGNAL FROM THE CELL SURPACE TO THE NUCLEUS.
-!- SIGNAL FROM THE CELL SURPACE TO THE NUCLEUS.
-!- SUBUNIT: ACTIVE ISGF3 CONSISTE OF TWO COMPONENTS, A REGULATORY MULTISUBUNIT COMPLEX, ISGF3 ALPHA (COMPONENTS, A REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Transcriptional regulator ISGF3 gamma subunit (IFN-alpha responsive transcription factor subunit) (Interferon stimulated gene factor 3 gamma) (ISGF3 p48 subunit) (ISGF-3 gamma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=92334329; PubMed=1630447;
Veals S.A., Schindler C., Leonard D.G.B., Fu X.-Y., Aebersold R.H.,
Darnell J.E. Jr., Levy D.E.;
Subunit of an alpha-interferon-responsive transcription factor is
related to interferon regulatory factor and Myb families of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                 Indels 159;
           Length 424;
                                                                                                                                                                                  ---APAG--
           DB 1;
                                 152;
                       .6e-12;
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                                65; Mismatches
           Score 333.5;
Pred. No. 1.6
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          12.2%;
24.3%;
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                      Similarity
                                121;
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          Query Match
Best Local 8
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                                 Matches
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 CTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQLWAR 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 RMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRG-SPRY 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGEAAAPESPHQAE----PYLSPSPSACTAVQEPSPG-ALDVTIMYKGRTVLQKVVGHPS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
AND STAT2, ALSO DESIGNATED P91/P84 AND P113 RESPECTIVELY) AND ISGF3 GAMMA (OR P48). THEY ASSEMBLE WHEN THE ISGF3 ALPHA COMPONENT IS PHOSPHORYLATED VIA INF ACTIVATION. SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                       the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 WLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSE-ADARIFKAWAVARGRWPPSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 WVVEQVESGQFPGVCWDDTAKTMFRIPWKHAGKQDFREDQDAAFFKAWAIFKGKY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQSCLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 HILTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQPAALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00267; INTPRNREGFCT.
ProDom; PD002355; IRF; 1.
PROMO348; IRF; 1.
PROSITE; PS00601; IRF; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein;
                                                                                                                              INDUCTION: BY IFW-ALPHA AND IFW-BETA. UPON STIMULATION THE REGULATORY PHOSPHORYLATED ALPHA AND BETA SUBUNITS ASSEMBLE WITH GAMMA SUBUNIT AND TRANSLOCATE FROM THE CYTOPLASM TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-SER.
F8E3784354BFD4A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRYPTOPHAN PENTAD REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.0%; Score 328.5; DB 1; 25.7%; Pred. No. 2.8e-12; iive 69; Mismatches 179;
                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE IRF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43696 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M87503; AAA58687.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001346; IRF. Pfam; PF00605; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSFAC; T01456; -. Genew; HGNC:6131; ISGF3G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 EWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLS-EADARIFKAWAVARGRWPPSS 74
                                                                                                                                                                                                                                                                                                                                                                Schmidt M., Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION OF TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON CONSENSUS SEQUENCE (ICS)). PLAYS A NEGATIVE REGULATORY ROLE IN CELLS OF THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                     "Human interferon consensus sequence binding protein is a negative regulator of enhancer elements common to interferon-inducible
                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-Lung, and Monocytes;
TISSUE-Lung, and Monocytes;
Weisz A., Marx P., Sharf R., Appella E., Driggers P.H., Ozato K.,
Levi B.-Z.;
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.3%; Score 308.5; DB 1; Length 426; 21.8%; Pred. No. 4.2e-11; cive 71; Mismatches 161; Indels 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBCELLULAR LOCATION: Nuclear.
-:- TISSUE SPECIFICITY: PREDOMINANTY IN LYMPHOID TISSUES.
-:- INDUCTION: BY INTERFERON GAMMA.
-:- SIMILARITY: BELONGS TO THE IRF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00348; IRF; 1.
PROSTITE; PS00601; IRF; 1.
Transcription regulation; DNA-binding; Nuclear protein;
Interferon induction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 110 TRYPTOPHAN PENTAD REPEAT.
426 AA; 48356 MW; 1535D1B7C83E0355 CRC64;
                               01-JUL-1993 (Rel. 26, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Interferon consensus sequence binding protein (ICSBP).
   426 AA
                                                                                                                                                                                                                                                                                                      genes.";
J. Biol. Chem. 267:25589-25596(1992).
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001346; IRF.
Pfam; PF00605; IRF; 1.
PRINTS; PR00267; INTFRNREGFCT.
ProDom; PD002355; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M91196; AAB63813.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 21.83
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSFAC; T02038; -. Genew; HGNC:5358; ICSBP1.
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A45064; A45064.
                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P23906; 2IRF
                                                                                                                                                         NCBI_TaxID=9606;
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   HUMAN
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Best Local &
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                   Q02556;
                원
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75 RGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYALSRELCWREG 133

-----KEGDKAEPATWKTRLRCALNKSPDFEEVTDRSQLDISEPYKVYRI

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134 PGTDQTEAEAPAAVPPPQGGPPGFFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQSC-- 191
                                                                               113 --VPEEEQKCKLGV---------ATAG----CVNEVTEMECGR 140
                                                                                                                                                                                                                                           ----PSVDDYMGMIKRSPSP---- 165
                                                                                                                                                                                                                                                                                                                                                                                                                            166 -----TOPTHER 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 ---LDVTIMYKGRTVLQKVVGHP-SC-----TFLYGPPDPAVRATDPQQVAFPS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 FSQMVISFYYGGKLVGQATTTCPEGCRLSLSQPGLPGTKLYGP-----EGLELVRFPP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 PAELPDOKOLRYTEELLRHVAPGLHLELRGPOLWARRMGKCKVYWEVGGPPGSASPSTPA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 CLLPRNCDTPIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKL 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 --LERDEVVQVFDTSQFFRELQQFYNSQGR-LPDGRVVLCFGEEFPDMAPLRSKLILVQI 369
                                                                                                                                                               192 -LADHLLTASWGADPVPTKAPGEQEGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQP
                                                                                                                                                                                                                                                                                                                                    251 AALTTGEAAAPESPHQAEPYLSPSPSACTA-----VQEPSPGA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      454 EPWLCRVHLEGTQREGVSSLDSSDL-------DLCLSSANSLY 489
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Search completed: June 18, 2003, 12:47:06 Job time : 17 secs

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June 18, 2003, 12:43:22 ; Search time 36 Seconds (without alignments) 2878.936 Million cell updates/sec
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1 MALAPERAAPRVLFGEWLLG......SANSLYDDIECFLMELEQPA 503
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9ue79 homo sapien	Q90zd4 gallus gall	Q9hb64 homo sapien	057578 xenopus lae	Q9n136 ovis aries	Q91vd0 mus musculu	Q8wnq4 sus scrofa	Q96gl3 homo sapien	Q98tx7 gallus gall	Q98tx6 gallus gall	Q99419 homo sapien	Q90wi0 gallus gall	Q9qz17 mus musculu	Q924t6 mus musculu	Q9rkr9 streptomyce	O98tal fign mbrin
SUMMARIES	ID	Q9UE79	Q902D4	Q9HB64	057578	Q9N136	Q91VD0	Q8WNQ4	Q96GL3	Q98TX7	Q98TX6	Q99419	OIMO6Ö	Q9QZL7	. Q924T6	Q9RKR9	O98TA1
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de	Query Match	40.9	28.5	22.1	16.1	15.7	15.7	15.4	13.3	13.3	13.3	12.6	11.8	10.3	7.1	6.7	6.5
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61 APGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQE 120

354 APGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQE

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175 173.5 168.5 168.5 168.5 168.5 168.5 168.5 167.5 16	Q90584 gall Q9bg75 ovis	09n137 o 09pwi9	Q923e9 mus musculu Q8r4e0 sigmodon hi	069270		Q95290 Bus BC	Obziac	041935 murid 090ww5 ctenoi		Q9y6i3 homo sapien	091213 091390		Q9gky7 oryctolagus	9apa60	Qessa		Q9D139 IIOMO Q9ha18 homo	Q8qzt8 mus	023635 caenc	9 Q9et79 mus musculu 2 Q9esq2 mus musculu	ALIGNMENTS	210 AA.	વિ	ed)	sequence update/ annotation update/	factor 7C.2.		Craniata; Vertebrata; Euteleostomi;	ноштигае;						y factor associated with Epstein-			45895671CEAA18F5 CRC64;	1116: DB 4	No. 9.5e-70; matches 2; Indels	MYKGRTVLOKVVGHPSCTFLYGPPDPAVRATDPOOVAFPSPAELPDOKOLRYTEELLRHV 353	)	
176 173.5 168.5 168.5 168.5 168.5 168.5 167.5 16	m																		8	00	ALI	PRT;		Creat	s, nast 6. Last	ory fa	l						9315633;	,	regulator		5757 (1997	Μ.		Pre 0,	CTFLYGPPD		1111111111
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                                                 Q9HB64
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  RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 DSTEGVAAAALTQVDLDLLQSVLQHCNISAL----GSQPTLWAHTGDALPEDALLLLPGQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ACAGGPGLPAGELYGW-AVETTPSPGPQP-----AALTTGEAAAPESPHQAEP 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 DGCLPGP-----QFQDWRQLEEPLLLGNQPLTGGGCGQDGAGALPVSEECAIPAPSPAEE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 YL----SPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVGHPSCTFLYGPPDPAVRATD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 LIFQSANPAPPPPAGDIGGLPPLLDITIYYRGKMVYQEQVDDSRCVLAYQPLDPAV--AE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 PQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEV---- 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   441 GRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDLCLSSANSLYDDIECFLMELE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YALSRELCWREGPGTDQTEAEAPAAVPPPQ--GGP------PGPFLAHTHAGLQ---- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAVA------SGVPNDRGSGGPVAGALQQQPQLLLNHHDLALENTPT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ALAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -APGPLPAPAGDKGDL-LLQAVQQSCLADHLLTASWGADPVPTKAPGEG--QEGLPLTG-
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
May D.L., Grant C.E., Deeley R.G.;
"Cloning and Promoter Analysis of the Chicken Interferon Regulatory
Factor-3 Gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.5%; Score 778; DB 13; Length 49
38.5%; Pred. No. 5.5e-46;
ive 59; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Factor-3 Gene.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF268079; AAK58583.1; -. InterPro; IRR001346; IRF. InterPro; IRR001346; IRF. Pfam; PP00605; IRF; 1. PROSITE; PS00601; IRF; UNXNOWN 1. SEQUENCE 491 AA; 54440 MW; 90E0C80A2624B1B4 CRC64;
                                                                                                                                                                                                                        (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                            DSSDLDLCLSSANSLYDDIECFLMELEQPA 503
                                                                                                                                                                              491
                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                      Interferon regulatory factor-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 38.5
les 208; Conservative
                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
                                                                                                                                                                                                                           01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                               01-MAR-2002
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  474
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=2049357; PubMed=10924517;

MEDLINE=20493557; PubMed=10924517;

Lu R., Au W.-C., Yeow W.-S., Hageman N., Pitha P.M.;

Lu R., Au W.-C., Yeowoter activity of interferon regulatory factor-7 gene. ACTIVATION BY INTERFERON AND SILENCING BY HYPERMETHYLATION.";

J. Biol. Chem. 275:31805-31812 (2000).

EMBL; AF277159; AAG30003.1;

HSSP; P23906; 21RR.

InterPro; IPR001346; IRF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 RAAPRVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "An interferon regulatory factor-related gene (xIRF-6) is expressed the posterior mesoderm during the early development of Xenopus
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98086218; PubMed=9426249;
Hatada S., Kinoshita M., Takahashi S., Nishihara R., Sakumoto H.,
Fukui A., Noda M., Asashima M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 RGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 AA; 14363 MW; 09B5B6F3CC11BB15 CRC64;
                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Interferon regulatory factor-7H (Fragment)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.1%; Score 603; DB 4; L ilarity 100.0%; Pred. No. 1.5e-34; Conservative 0; Mismatches 0;
128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam, PF00605; IRF; 1.
PRINTS; PR002357; INTFNREGFCT.
ProDom, PD002355; IRF; 1.
SMART; SMO0348; IRF; 1.
PROSITE; PS00601; IRF; 1.
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ProDom; PD002355; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 203:183-188(1997).
EMBL; D86492; BAA24349.1;
HSSP; P23906; 2IRF.
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Pfam; PF00605; IRF; 1.
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PRELIMINARY;
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SMART; SM00348; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI TaxID=9606;
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Similarity
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                                                                        141;
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Query Match
Best Local S
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                                    Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGDLLLQAVQQSCLADHLLTASWGADPVPTKAP-----GEGQEGLPLTGACAGGPGLPA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GELYGWAVETTPSPGPQPAAL--TTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALD 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 -----PEQIWPKTEPQEMEVPPTSGPADFFSSP---EWMISSLPMT------DLE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 VTIMYKGRTVLQKV-VGHP-SCTFLYGPPDPAVRATD-----PQQVAFPSPAELPDQKQ 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 IQFYYRGKEMGÓTMTVSNPQGCRLFYGDLGPMPNQEELFGPITLEQVRFPGTEQIVNEKÓ 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        403 PIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHL 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| :|: :|: |: |: |: 334 KLFCVETFLSDLISHQKGIITKQPPYEIYLGFGEEWPDGKYKERKLIIVQIIPIVARMII 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDT 402
                                                                                                                                                                                                                                               29
                                                                                                                                                                                                                                                                                                                26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 HKVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDDFEADELNQS------QNHVPISEPFNCLNINDSPIGSSSTGSCT----
                                                                                                                                                                                                                                           1 MALAPERAAPRVLFGEWLLGEISSGCYEGLOWLDEARTCFRVPWKHFAR-KDLSEADARI
                                                                                                                                                                                                                                                                                                                                                                                         FKAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGD-PADP
                                                                                                                                                                                                                                                                                                                MAMHPR----RVRLKPWLVAQVDSGMYPGLIWLNREAKRFQIPWKHATRHSPRQEEENTI
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interferon regulatory factor 6.
Ovis aries (Sheep).
Bukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                     Query Match 16.1%; Score 440; 'DB 13; Length 459; Bet Local Similarity 27.1%; Pred. No. 1.1e-22; Aatches 140; Conservative 74; Mismatches 197; Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-15 DAY PRECNANT UTERUS;
Choi Y., Spencer T.E., Bazer F.W.;
"Cloning and Analysis of Ovine IRF-6.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP234446; AAF34782.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348; IRF; 1.
:00601; IRF; 1.
467 AA; 52970 MW; 21E04F749844D88F CRC64;
PROSITE; PS00601; IRF; 1.
SEQUENCE 459 AA; 52475 MW; 306DA77C6586871C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGTQREGVSSLDSSDLDLCLSSANSLYDDIECFLMEL 499
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Pfam; PP00605; IRF; 1.
PRINTS; PR000567; INVFRNREGFCT.
ProDom; PD002355; IRF; 1.
SMART; SM00348; IRF; 1.
PROSITE; PS00601; IRF; 1.
SEQUENCE 467 AA; 52970 MW; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 NDVDEEDEEDELDQSQHHVPIQDTFPFLNINGSPI---APGS-----'VGNCSVGNCSP 188
                                                                                                                                                                                                                     60 FKAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGD-PADP 118
                                                                                                                                                                                                                                                                            107
                                                                                                                                                                                                                                                                                                                                119 HKYYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLP---- 173
                                                                                                                                                                                                                                                                                                                                                                                     108 VKIY----QVC-------DIPQPQGSIINP------GSTGSAPWDEKD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAV---W-----PKTEPLEMEVPQ--APIQPFYSSPELWISSLPMT------DLDI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 TIMYKGRIVLQKV-VGHP-SCTFLYGPPDP-----AVRATDPQQVAFPSPAELPDQKQL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 RYTEELLRHVAPGLHLELRGPOLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTP 403
                                                                                                                                                               26
                                                                                                                                                                                                                                                     1 MALHPR----RVRLKFWLVAQVDSGLYPGLIWLHRDSKRFQIPWKHATRHSPQQEEENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                              174 --APAGDKGDLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 AGELYGWAVETTPSPGPOPAALTIGEAAAPESPHQAEPYLSPSPSACTAVOEPSPGALDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 IFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLE
                                                                                                        1 MALAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFAR-KDLSEADARI
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                    94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 467;
15.7%; Score 430; DB 6; Length 46
27.3%; Pred. No. 5.7e-22;
cive 72; Mismatches 209; Indels
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL365322; CAC42184.1; -.
EMBL; EC008515; AAH00515.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
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InterPro; IPR001346; IRF.
Promon; PD00235; IRF; 1.
PRODON; PD002355; IRF; 1.
SEQUENCE 467 AA; 53110 MW; IC564BC8D79C5259 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
BM282D4 4 (interferon regulatory factor 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405 MFSGDFTRSFDSGSVRLQISTPD-IKDNIVAQLKQL 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464 GTQREGVSSLDSSDLDLCLSSANSLYDDIECFLMEL 499
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Pred. No. 7.8e-22;
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27.5%;
                                                         Conservative
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Submitted (APR-2001)
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                                                                                                                                                                                                                                                                                                                        114 C------DIPOPQG-----SVVNPGSTGSAPWDEKD---NDVD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 DEDEEDE-LDQSQHHVPIQDTFPFLNINGSPIAPASVDNCSVGNCSPEAV---W----- 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 SPGPQPAALTIGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVLQKV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 -VGHP-SCTFLYGPPDP----AVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPG 356
242 TVSNPQGCRLFYGGLGPMPDQEELFGPVSLEQVKFPGPEHITNEKQKLFTSKLLDVMDRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 HOKGOIEROPPFEIYLCFGEEWPDGKPLERKLILVQVIPVVARMIYEMFSGDFTRSFDSG
                                                                                                                70 WPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGD-PADPHKVYALSREL
                                                                                                                                                            189 QSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGA----CAGGPGLPAGELYGWAVETTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 -PKAEPLEMEVPQ--APIQPFYSSPELWISSLPMT-----DLDIKFQYRGKEYGQTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 FRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSS
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01-DEC-2001 (TrEMBLrel. 19, Last seg
01-MAR-2002 (TrEMBLrel. 20, Last ann
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Submitted (JUN-2001) to the
EMBL; BC009395; AAH09395.1;
InterPro; IPR001346; IRF.
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TISSUE=BRAIN;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 EKDNDVDEDEE----EDELEQSQHHVPIQDTFPFLNINGSPMAPASVGNCSVGNCSP--- 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------EŚVWPKTEPLEMEVPQAPIQPFYSSPELWISSLPMT------DLDIKFQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                               59
                                                                                                                                                                                                                                                                 108 VXIY----SVC-----DIPQTQG-----DIPGTGSAPWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HKVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYGWAVETTPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKGRTVLOKV-VGHP-SCTFLYGPPDP----AVRATDPOQVAFPSPAELPDQKQLRYT
                                                                                                                       FKAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGD-PADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGDLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPL----TGACAGGPGLPAGE
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                                                                            1 MALAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFAR-KDLSEADARI
              Gaps
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Sus.
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              88;
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          212; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00348; IAE; ...
PROSITE; PS00601; IRE; UNKNOWN 1.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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          Mismatches
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          72;
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PRINTS; PR00267; INTFRNREGFCT.
ProDom; PD002355; IRF; 1.
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01-MAR-2002 (TrEMBLrel. 20, L
01-JUN-2002 (TrEMBLrel. 21, L
Interferon regulatory factor
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Matches 138; Conservative
          141; Conservative
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          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 WPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSRELC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 WREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQ 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 452;
                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butel.
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases
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Pfam; PP00605; IRF; 1.

Proposite; PS00601; IRF; UNKNOWN 1.

PROSITE; PS00601; IRF; UNKNOWN 1.

PROSITE; PS00601; IRF; UNKNOWN 1.

PROSITE; PS00601; IRF; UNKNOWN 1.

PROFITE; PS00601; IRF; UNKNOWN 1.
                                                                              01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Similar to interferon regulatory factor 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.3%; Score 364.5; DB 4;
llarity 27.4%; Pred. No. 1.8e-17;
Conservative 43; Mismatches 153;
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Db 224 TPGIPIEPSIRSGBALALSDCRLHICLYYREMLVKEV 260  304 VVGHP-SCTFLYGPPDFAVRATDPQQVAFPSPAELPDQKQLRYTEELLBHVAPGLHLELR 362.  261 TTSSPEGCRISQGGSYEVSSLEQVIPPYPEDNOGRANIEKLLSHLERGVILWMA 314  Qy 363 GPQLWARRWGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIPPRRVFFQELVEPRAR 420  Db 315 PDGLYAKRLCQSRIYWDGPLALCSDRPNKLERDQTCKLFDTQQFLAELQAF-AH 367  Qy 421 QRRGSPRYTIXLGFQQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDL 480  Db 368 HGRPLPRYQVALCFGEBEPDPQ-RQRKLITAHVEPWFARQLYYFAQQNSGHLLRGYDLPE 426  Qy 481 CLSSANSLYDDI 492  ::	RESULT 10  Q98TX6  ID Q98TX6  PRELIMINARY; PRT; 409 AA.  AC Q98TX6;  O1-UNA-2001 (TrEMBLrel: 17, Last sequence update)  DT 01-UNA-2001 (TrEMBLrel: 17, Last sequence update)  DT 01-UNA-2001 (TrEMBLrel: 19, Last annotation update)  DR 10-DR 1	Query Match         13.3%; Score 362; DB 13; Length 409;           Best Local Similarity         25.0%; Pred. No. 2.4e-17;         Indels 126; Gaps 18           Qy         16 EMLLGEISSGCYEGLQMLDEARTCFRVPWKHFARKDLS-EADARIFKAMAVARGRWPPSS 74         16 :
	RESULT 9 098TX7 AC 098TX7 DT 096TX7 DT 0-30TX201 (TrEMBLrel. 17, Created) DT 01-JUN-2001 (TrEMBLrel. 17, Created) DT 01-JUN-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) C C Actors auxia, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; C C Archosauria, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; C Archosauria, Aves; Neognathae; Galliformes; Phasianinae; C Archosauria, Newpou N.A. RC STRAIN-ESPARA; TISSUE-SPLEEN; RX MEDINES-1424622; PubMed=1153327; RX MEDINES-1424622; PubMed=1153327; RX MEDINES-1424622; PubMed=1153327; RX MEDINES-142622; PubMed=1153327; RX MEDINES-142623 PubMed=1153327; RX MEDINES-142623 PubMed=1153207; RX MEDINES-142623 PubMed=1153327; RX MEDINES-142622 PubMed=1153327;	Query Match         13.3%; Score 364; DB 13; Length 445;           Best Local Similarity         26.4%; Pred. No. 1.9e-17;           Matches 130; Conservative 71; Mismatches 201; Indels 90; Gaps 20;           Qy         16 EWLLGEISSGCYEGLQWLDEARTCRRVPWKHFARKDLS-EADARIFKAWANARGRWPPSS 74           :     :                 : : :

	Qy 300 VLQKVVGHP-SCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLH 358	Qy 359 LELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVE 416	Oy 417 FRARQRRGSPRYTIYLGFGQD 437 	RESULT 12 Q90WIO ID Q90WIO PRELIMINARY; PRT; 416 AA.	AC 2004W10; DEC-2010 (TERMELAE). 19, Created) DT 01-DEC-2010 (TERMELAE). 19, Last sequence update) DT 01-DEC-2010 (TERMELAE). 19, Last sequence update) DT 01-MAR-2002 (TERMELAE). 10, Last amnotation update) CM 101-MAR-2002 (TERMELAE). 10, Last amnotation update) CM 101-DEC-2010 (TERMELAE). 10, Last amnotation update) CM 102-DEC-2010 (TERMELAE). 10, Last amnotation update) CM 102-DEC-2010 (TERMELAE). 10, Last amnotation update) CM 102-DEC-2010 (TERMELAE). 11-DEC-2012 (TERMELAE). 11-DEC-2012 (TERMELAE). 11-DEC-2012 (TERMELAE). 11-DEC-2012 (TERMELAE). 11-DEC-2013 (TERMELAE). 11-	QY 301 LQKVVGHPSCTPLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLH 358
	Oy 304 VVGHP-SCTFLYGPPDPAVRATDPQQVAPPSPAELPDQKQLRYTEELLRHVAPGLHLELR 362	Qy 363 GPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRAR 420	Qy 421 QRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDL 480	Qy 481 CLSSANSLYDDI 492   ::	RESULT 11  Op9419  PRELIMINARY; PRT; 440 AA.  D9 09949  D 099419  D 0 099419  D 0 099419  D 0 099419  D 0 01-MAY-1997 (ITEMBLEG. 03, Last sequence update)  D 01-MAY-1997 (ITEMBLEG. 03, Last sequence)  D 113 REGIONDRAEAPAAVPENGEGERPEARENCESCOLINGARDEENCESCOLINGARD SEQUENCESCOLINGARD SEQUENCESCO	204LDRSW-RDYVPDQPHPEIPYQCPMTFGPRGHHWQGPACENGCQV-TGTFYACAP 241 ETTPSPG-PQPAALITGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRT

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17 WLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSE-ADARIFKAWAVARGRWPPSSR 75
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |::::||:|||||||:::|
15 WIVEQVESGHFPGVCWDDAAKTIMFRIPWKHAGKQDFREDQDAAIFKAWALFKEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-129/SVJ;
MEDLINE-21243724; PubMed=11345588;
Yawata M., Murata S., Tanaka K., Ishigatsubo Y., Kasahara M.;
Yawata M., Murata S., Tanaka K., Ishigatsubo Y., Kasahara M.;
'Nucleotide sequence analysis of the -35-kb segment containing
interferon-gamma-inducible mouse proteasome activator genes.";
Immunogenetics 53:119-129(2001).
EMBL; AB053120; BAB47407.1; -.
EMBL; AB053120; BAB47407.1; -.
EMGD; MGI:107587; Isgf3g.
InterPro; IPR001346; IRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 GGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSG-DPADPHKVYAL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----HKDGDIGHPAVWKTRLRCALNKSSEFEEVPERGRMDVAEPYKVYRI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2);
Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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Seeger K.J., Harris D.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prodom; PD002355; IRF; 1.
PROSITE; PS00601; IRF; UNKNOWN 1.
SEQUENCE 215 AA; 24028 MW; 5C2004D507F0C64D CRC64;
                                                                                                                                                                                                   (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Putative multi-domain regulatory protein.
SC02259 OR SCC75A.05C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
      297 KVYWSGPCAPSLAAPN----LIERQKKVKLFCLETF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.1%; Score 194; DB 11;
35.5%; Pred. No. 4.7e-06;
tive 21; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1334 AA
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                                                                                                                                                   PRT;
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 35.5
les 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor.
                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                      01-DEC-2001 (01-DEC-2001 (01-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
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                                                                                                                                                   0924T6
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                                                                                          RESULT
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                                                                                                                     Q924T6
      g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LELRGPQLWA-----RRMGKCKVYWEVGGP--PGSASPSTPACLLPRNCDTPIFDFRV 409
                                    410 FFQELVEFRARQRRGSPRYTIYLGFGQD--LSAGRPKEKSLVLVKLEPWLCRVHLEGTQR 467
                                                                                                                                                   88 RAGWKTNFRCALRSTRRFVMLRDNSGD-PADPHKVYALSRELCWREGPGTDQTEAEAPAA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 VPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQSCLADHLLTASWGADPV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 QPFYSSPELWISSLPMT-----DLDIKFQYRGKEYGQTMTVSNPQGCRLFYGDLGPM 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----AVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQLWARRMGKC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 QDTFPFLNINGSPMAPASVGNCSVGNCSP------ESVWPKTEPLEMEVPQAPI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 GLOWLDEARTCFRVPWKHFAR-KDLSEADARIFKAWAVARGRWPPSSRGGGPPPEAETAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---WKAQLRCALNKSREFNLMYDGTKEVPMNPVKIY----QVC-------D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 SPHQAEPYLSPSPSACTAVQEPSPGALDVIIMYKGRTVLQKV-VGHP-SCTFLYGPPDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.3%; Score 281.5; DB 11; Length 330; 26.0%; Pred. No. 6.9e-12; ive 49; Mismatches 161; Indels 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sands A., Mak T.W.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, PR177668; AAF00915.1; -.
INTERPRO, 21RF.
INTERPRO, IPR001346; IRF.
PRINTS, PR00265; IRF; 1.
PROMO, PR002355; IRF; 1.
PROST, SM00348; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 330
330 AA; 37355 MW; EB02EC8B751CBD7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, 17, 12f6 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Mouse)
                                                                                                                                                                                                                              468 EGVSSL 473
                                                                                                                                                                                                                                                                                          386 LGPALL 391
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   359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
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Gaps

Indels

Length 215;

Kinashi H., Hopwood D.A.;

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- PLDEPLQALRILRALRDSGRTAEALAAYEAVRR--LLADRLGTDPGPELRTLHAELLSPS 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHKVYALSRELCWREGP-----GTDQTEAEAPAAVPPPQGGP-PGPFLAHTHAGL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 PTPTPGRSRTPGWTSGPGPASGAGAASGTDVASGAGAASGPDPASGPASGPAVAPGSGGG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 QAPGPLPAPAGDKGDLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 PAPGWWPAPGTAPGSSTAPPHDTASAAD---TA---PAPGPTSAPGTA----PAAGTAAP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 APGTAGPAPGTSYAPGTAPVAGTTPAPGTAPAPGTAGPARDTSYAPGTAPVAGTTPAPGT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 GPGL--PA-GELY--GWA--VETTPSPGPQPAALTTGEA-----AAPESPHQAEPYL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPSPSACTAV-----QEPSPGALDVTIMYKGRTVLQKVVGHPSCTFLYGPPDPAVRAT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APAPGSTPAPGTVPAPGTAPAPGPQPA----DGR----RPVTGPASGT----GPG----AAT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 LLGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVARGRWPPSSRGG 77
         "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                   STRAIN=A3(2) / M45.

STRAIN=A3(2) / M45.

STRAIN=A3(2) / M45.

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Bentley S.D., Chater K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the model actinomycete Streptomyces coelicolor {\rm A3}\,(2)\,.\,",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPPPEAETAER-----AGWKTNFRCALRSTRRFVMLRDNSG-DPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.7%; Score 183; DB 16; Length 1 Best Local Similarity 28.1%; Pred. No. 0.00021; Matches 106; Conservative 25; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00364; DISEASERSIST.
PRINTS; PR01574; TUBBYPROTEIN.
ProDom; PD000329; Trans_reg_C; 1.
SEQUENCE 1334 AA; 138787 MW; 78DC746883E8778C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: June 18, 2003, 12:47:49 Job time : 39 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR005158; BAD.
Interpro; IPR000767; Disease_resist.
Interpro; IPR001867; Trans_reg_C.
                                                                                                                                                                                                                                                                                                                                                                                                                      CAB61705.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                     Nature 417:141-147(2002)
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version 5 - 2005 (
GenCore (c) 1993
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- protein search, using sw model OM protein May Run on:

6, 2005, 16:45:44 ; Search time 180 Seconds (without alignments) 1430.977 Million cell updates/sec

US-09-647-965-9 2731 Perfect score:

1 MALAPERAAPRVLFGEWLLG......SANSLYDDIECFLMELEQPA 503

Sequence:

Scoring table:

1612378 segs, 512079187 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Q92985 homo sapien	P70434 mus musculu	Q9ue79 homo sapien	Q90643 gallus gall	gallus	Q9hb64 homo sapien		carae	homo	рошо	Q64gb2 homo sapien	Q14653 homo sapien	sus E	Q7zxg6 xenopus lae	brac	P56477 mus musculu	O57578 xenopus lae		P70671 mus musculu	Q6gr23 xenopus lae	P97431 mus musculu	_	_	Q91vd0 mus musculu	Q63zp8 xenopus lae		Q8wnq4 sus scrofa	Q64ga9 homo sapien	mus m	7 brach	Q96gl3 homo sapien
SOMMAKIES	ΙD	IRF7 HUMAN	IRF7 MOUSE	Q9UE79	IRF3_CHICK	Q902 <u>D</u> 4	Q9HB64	Q6PE40	0802Н9	IRF5 HUMAN	QGRCMB	Q64GB2	IRF3 HUMAN	Q764M6	Q7ZXG6	Q6PGZ7	IRF5 MOUSE	057578	Q6NZY9	IRF3 MOUSE	Q6GR23	IRF6_MOUSE	IRF6_HUMAN	Q9N136	Q91VD0	Q63ZP8	Q6DD26	Q8WNQ4	Q64GA9	IRF4_MOUSE	Обрнк7	Q96GL3
	DB	! !	Н	~	н	~	~	~	~	-	7	~	-	7	~	~	-	~	~	-	7	Н	٦	7	~	7	7	~	~	٦	7	7
	Query Match Length	503	457	210	491	491	128	423	421	498	488	514	427	419	466	492	497	459	382	419	460	467	467	467	467	517	460	467	413	450	423	452
df	Query Match	99.4	57.2	40.9	28.6	28.5	22.1	19.0	18.9	17.9	17.7	17.7	16.8	16.6	16.4	16.3	16.3	16.1	16.1	16.0	16.0	•	15.8	15.7	15.7	15.5	15.5	15.4	14.6	•	13.5	13.3
	Score	2715	1562	1116	780	778	603	$\sim$	515.5	487.5	484.5	482.5	458	453.5	448	445.5	444.5	440	439.5	438	436.5	436	431	430	428	424	422.5	420	398	376	368	364.5
	Result No.	7	8	n	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27		29		31

Q72596 homo sapien Q98tx7 gallus gall Q15306 homo sapien Q98tx6 gallus gall Q99419 homo sapien Q90811 gallus gall P23611 mus musculu Q6ny63 brachydanio Q00978 homo sapien Q6ns16 xenopus lae Q90wi0 gallus gall Q64gbb homo sapien Q64gb homo sapien Q64gb homo sapien G0556 homo sapien	ratto
Q725G6 Q98TX7 IRF4 HUMAN Q98TX6 Q99419 ICSB CHICK ICSB MOUSE Q6NY63 Q6NS16 Q90MIO Q6AGNONIO	Q68FP4
001001101000F	1 (2)
4 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6	398
11122.124.00.12.13.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3	11.2
364.5 364.5 363 362 344 333.5 323.5 328.5 328.5 328.5 328.5	306
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## ALIGNMENTS

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Name=C; Synonyms=Gamma; Isold=0292985-3; Sequence=VSP_002758, VSP_002759; Note=May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
Hillman R.T., Green R.E., Brenner S.E.;
"An unappreciated role for RNA surveillance.";
Genome Biol. 5:RESPARCH008.1.RESEARCH008.16(2004).
-!- FUNCTION: Transcriptional activator. Binds to the interferonstimulated response element (ISRE) in IFN promoters and in the promoter (Qp) of EBV nuclear antigen-1 (EBNAI).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97459673; PubMed=9315633;
Zhang L., Pagano J.S.;
IRR-7, a new interferon regulatory factor associated with Epstein-
Barr virus latenoy.";
                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM D).
MEDLINE=99003279; PubMed=9786932; DOI=10.1074/jbc.273.44.29210;
ALW W.-C., MOORTE P.A., LaFleur D.W., Tombal B., Pitha P.M.;
ALW A.C., MOORTE P.A., LaFleur D.W., Tombal B., Pitha P.M.;
"Characterization of the interferon regulatory factor-7 and its
potential role in the transcription activation of interferon A
                                                                                                                                                                                                                                                                                     Grossman A., Nicholl J., Antonio L., Luethy R., Suggs S., Sutherland G.R., Mak T.W.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=4;
                                   092985; 000331; 000332; 000333; 075924;
01-N0V-1997 (Rel. 35, Created)
N-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                     503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=A;
IsoId=Q92985-1; Sequence=Displayed;
Name=B; Synonyms=Beta;
IsoId=Q92985-2; Sequence=VSP_002760;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
                                                                                                               Interferon regulatory factor 7 (IRF-7)
Name=IRF7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 273:29210-29217(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Cell. Biol. 17:5748-5757(1997).
                   PRT;
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM A). TISSUE=Spleen;
                   STANDARD;
                                                                                                                                                      Homo sapiens (Human)
                     HUMAN
HUMAN
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                        Name=1rf7;
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                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tryptophan pentad repeat.
MALAPE -> MPVPERPAGFDSPRPGTR (in isoform
          Isold=Q92985-4; Sequence=VSP_002757;
TISSUE SPECIFICITY: Expressed predominantly in spleen, thymus and peripheral blood Leukocytes.
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                                                                                                                                                                                                                                                               |, 605047; -. Grytoplasm; TAS. G0:0005034; C:uucleus; ISS. G0:0005634; C:uucleus; ISS. G0:0005634; C:uucleus; ISS. G0:0005634; E:DNA binding; ISS. G0:000127; F:DNA binding; ISS. G0:0000122; P:inflammatory response; ISS G0:0000122; P:negative regulation of transcription from P. .; TJ G0:0006731; P:passive viral induction of host immune resp. .; TJ G0:000674; P:response to DNA damage stimulus; ISS. G0:0006615; P:response to virus; ISS. G0:000665; P:response to virus; ISS. G0:000667; P:response to virus; ISS.
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GGPPGPFLAHTHA -> AQGSLLGSCTGGQ (in
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Activator; Alternative splicing; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (in isoform C).
/FIId=VSP 002759.
Missing (in isoform B).
/FIId=VSP 002760.
E -> K (in Ref. 2).
Q -> R (in Ref. 3).
W; AAGA39E0E272727C CRC64;
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Pred. No. 1.8e-142;
1; Mismatches 2;
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                                           SIMILARITY: Belongs to the IRF family.
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/FTId=VSP 0
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Interpro; IPR008984; SMAD FHA.
Interpro; IPR009088; Wing_hix_DNA_bnd.
Pfam; PF00605; IRF; 1.
                                                                                                                                                       EMBL, U73036; AAB17190.1; -.
EMBL, U53830; AAB80686.1; -.
EMBL, U53832; AAB80688.1; -.
EMBL, U53832; AAB80650.1; -.
EMBL, AF076494; AAC70999.1; -.
TRANSFAC; T04674; -.
TRANSFAC; T05106; -.
Genew, AGNC:6122; IRF7.
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ProDom; PD002355; IRF; 1.
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DNA BIND 13 122
VARSPLIC 1 6
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503 AA;
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Best Local S
Matches 500
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SEQUENCE
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121 VYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDEG 180
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                                                                       DILLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAV
                                                                                                                                                                                                            ETTPSPGPOPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTV
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Grossman A., Nicholl J., Antonio L., Luethy R., Suggs S.,
Sutherland G.R., Mak T.W.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Transcriptional activator. Binds to the interferonstimulated response element (ISRE) in IFN promoters and in the Q promoter (Qp) of EBV nuclear antigen-1 (EBNA1) (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00348; IRF; 1.
PROSTIE; PS00601; IRF; 1.
Activator; DNA-binding; Nuclear protein; Transcription regulation.
DNA_BIND 11 122 Tryptophan pentad repeat.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
02-ULJ-2004 (Rel. 44, Last annotation update)
Interferon regulatory factor 7 (IRF-7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               457 AA
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Interpro; IPR008984; SMAD_FHA.
Interpro; IPR009058; Wing_hlx_DNA_bnd.
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PRINTS; PR00267; INTFRNREGFCT.
ProDom; PD002355; IRF; 1.
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HSSP; P23906; 1IRF.
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                                                                                                                                          61 APGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQB 120
                                                                                                                                                                                                                                                                  Grant C.E., Vasa M.Z., Deeley R.G.;
"CIRF-3, a new member of the interferon regulatory factor (IRF) family that is rapidly and transiently induced by dsRNA.";
Wucleic Acids Res. 23:2137-2146(1995).
-! FUNCTION: May activate transcription by complex formation with other transcriptional factors, possibly members of the STAT family. Binds specifically to the IFN-stimulated response element (ISRE) but not to the IFF-1 binding site PRD-I.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the IRF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no restrictions on ng as its content is in no
                                    MYKGRIVLQKVVGHPSCTFLYGPPDPAVRATDPQQVAPPSPAELPDQKQLRYTEELLRHV
                                                                                                                                                                                                                                414 IVEFRARORRGSPRYTIYLGFGODLSAGRPKEKSLVLVKLEPWLCRVHLEGTOREGVSSL
                                                                                                   354 APGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
PROSITE; PS00661; IRF; 1.
Activator; DNA-binding; Nuclear protein; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

28.6%; Score 780; DB 1; Length 491;
Best Local Similarity 38.5%; Pred. No. 1.7e-35;
Matches 208; Conservative 60; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tryptophan pentad repeat.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Interferon regulatory factor 3 (IRF-3)
Gallus gallus (Chicken)
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InterPro; IPR001346; SMAD_FHA.
InterPro; IPR0090894; SMAD_FHA.
InterPro; IPR009058; Wing_hlx_DNA_bnd.
Pfam; PP00605; IRF; 1.
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ProDom; PD002355; IRF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 MYKGRTVLQKVVGHPSCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHV 353
                                                                                                                                                                                                                                                                                                                                                                                            119
                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 KVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPGFFLAHTHAGLQAPGPLPAPAGDK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 KVYELSRELGSTVGPATENREEVSLSNALPTQGVSPGSFLARENAGLQTPSPL--LSSDA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 TVLQAVVGHPRCVFLYSPMAPAVRTSEPQPVIFPSPAELPDQKQLHYTETLLQHVSPGLQ 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFR 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 LELRGPSLWALRMGKCKVYWEVGSPMGTTGPSTPPQLLERNRHTPIFDFSTFFRELEEFR 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARORRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDL 478
                                                                                                                                                                                                                                                                                                                                WAVARGRWPPSSRGGGPPPEAETA---ERAGWKTNFRCALRSTRRFVMLRDNSGDPADPH 119
                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                       1 MAEVRGVQRVLFGDWLLGEVSSGQYEGLQWLNEARTVFRVPWKHFGRRDLDEEDAQIFKA
                                                                                                                                                                                                                                                                                                                                                                     GDLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELY-GW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 QVEAVPSPRPQQPALT-------ERSLGFLDVTIMYKGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 AVETTPSPGPQPAALTIGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGR
                                                                                                                                                                                                      3 LAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFKA
                                                                                                                                       Gaps
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"IRF-7, a new interferon regulatory factor associated with Epstein-Barr virus latency.";
Mol. Cell. Biol. 17:5748-5757(1997).
BMBL; US3832; AAB80691.1; -.
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                                                                                                                                       52;
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                                                                        Length 457;
                                                           57.2%; Score 1902,
62.6%; Pred. No. 9.2e-79;
tive 36; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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SEQUENCE 210 AA; 23592 WW; 45895671CEAA18F5 CRC64;
         51222 MW; 30B102C668F56142 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative interferon regulatory factor 7C.2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       479 DLCLSSANSLYDDIECFLMELEQ 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                      Best_Local Similarity 62.63
Matches 315; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 208; Conservative
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         457 AA;
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         SEQUENCE
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**Q9UE79** 

RESULT 3 **09UE79**  61 2 ALAPERAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFK

17;

92; Gaps

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NCBI_TaxID=9606;
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                                                               ||| | || || || AWAKASGRY------EGNAEDPAKWKTNFRCALRSTHMFMLLEDRSKCNDDPHKV 111
                                                                                                                                                                                    STEGVAAAAITQVDLDLLQSVLQHCNISAL----GSQPTLWAHTGDALPEDALLLPGQ 207
                                                                                                                                                                                                                        -ACAGGPGLPAGELYGW-AVETTPSPGPQP-----AALTTGEAAAPESPHQAEP 269
                                                                                                                                                                                                                                                     208 DGCLPGP----QFQDWRQLEEPLLLGNQPLTGGGCGQDGAGALPVSEECAIPAPSPAEE 262
                                                                                                                                                                                                                                                                                  YL----SPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVGHPSCTFLYGPPDPAVRATD 325
                                                                                                                                                                                                                                                                                                             263 LÍFQSANPAPPPAGDIGGLPPLÍDITÍYÝRGKMÝYQEQVDDSRCVLAÝQPLDPAV--AE 320
                                                                                                                                                                                                                                                                                                                                                           321 ORLVLFPSPASLPDPRORRYTEDLIE--VAGIRLEORAGOLLATRIKKCKVFWALSOOLE 378
                                                                                                       YALSRELCWREGPGTDQTEAEAPAAVPPPQ--GGP-----PGPFLAHTHAGLQ---- 167
                                                                                                                                     YAVA-----SGVPNDRGSGGPVAGALQQQPQLLLINHHDLALENTPT 152
                                                                                                                                                                                                                                                                                                                                                                                                                    432 TKPKESKLILVKLVPQFCEYWYEQVQRGGASSLNSGNVSLQLSDSFNLFELIEQYHWQTD 491
                                             AWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKV 121
61
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                                                                                                                                                                                                                                                                                                                                          POQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEV----
                                                                                                                                                                                                                                                                                                                                                                                                    GGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            441 GRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDLCLSSANSLYDDIECFLMELE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor activity; IEA.
transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 778; DB 2; Length 491; Pred. No. 2.2e-35; 59; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
May D.L., Grant C.E., Deeley R.G.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF268079; ARK58583.1; --
HSSP; P15314; 11F1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Interferon regulatory factor-3.
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GO; GO:0003700; F:transcription fa
GO; GO:000635; P:rgulation of tr
Pfam; PF00605; IRF; I.
PRINTS; PR00267; INFFNREGFCT.
ProDom; PD002255; IRF; I.
SMART; SM00348; IRF; I.
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SEQUENCE 491 AA; 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 LLFQSANPAPPPAGDIGGLPPLLDITIYYRGKMVYQEQVDDSRCVLAYQPLDPAV--AE 320
AWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKV 121
                                                                  63 AWAKASGRY-----EGNAEDPAKWKTNFRCALRSTHMFMLLEDRSKCNDDPHKV 111
                                                                                                                                            YALSRELCWREGPGTDQTEAEAPAAVPPPQ--GGP-----PGPFLAHTHAGLQ---- 167
                                                                                                                                                                                                                       -----SGVPNDRGSGGPVAGALOQOPOLLLNHHDLALENTPT 152
                                                                                                                                                                                                                                                                                                                                                                       153 DSTEGVAAAALTQVDLDLLQSVLQHCNISAL----GSQPTLWAHTGDALPEDALLLPGQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 PQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEV---- 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431
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EMBL, AR277159; AAG30003.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -ACAGGPGLPAGELYGW-AVETTPSPGPQP-----AALTTGEAAAPESPHQAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 YL----SPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVGHPSCTFLYGPPDPAVRATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 QRLVLFPSPASLPDPRORRYTENLLE--VAGLRLEORAGOLLATRLKKCKVFWALSQOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 GGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----PLNLLHRDQETTIFDFRVFCTELRDFRDSRRERSPDFTIFLCFGQCFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441 GRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDLCLSSANSLYDDIECFLMELE
                                                                                                                                                                                                                                                                                                     168 -APGPLPAPAGDKGDL-LLQAVQQSCLADHLLTASWGADPVPTKAPGEG--QEGLPLTG-
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GO; GO:0005634; C:nucleus; TAS.
GO; GO:0003677; F:DNA binding; TAS.
GO; GO:0003702; F:RNA polymerase II transcription factor acti...
GO; GO:0006934; P:Inflammatory response; TAS.
GO; GO:0066731; P:passive viral induction of host immune resp...
GO; GO:0006974; P:response to DNA damage stimulus; NAS.
GO; GO:000637; P:renscription initiation from Pol II promoter; InterPro; IPR001346; IRP.
InterPro; IPR001346; IRP.
PFGM; PF00605; IRF; 1.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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ProDom; PD002355; IRF; 1.
SMART; SM00348; IRF; 1.
PROSITE; PS00601; IRF; 1.
NON TER 128 128
SEQUENCE 128 AA; 14363 MW; (
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14363 MW; 09B5B6F3CC11BB15 CRC64;

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FGEWILGEISSGCYEGLOWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVARGR---W 70
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01-UUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
Interferon regulator factor
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
A plotting R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A papleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Richards S., Worley K.C., Hale S., Gardera A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Blakesley M., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
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                                                                                              RAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVA 79
                                                                    RAAPRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Straubberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC058298; AAH58298.1; -.
ZFIN; ZDB-GENB-404026-1518; irf7.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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                                                                                                                                        TISSUB=Kidney, MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                             RGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.0%; Score 520; DB 2; Length 423; 30.9%; Pred. No. 3.5e-21; ive 67; Mismatches 174; Indels
                Length 128;
                                          Indels
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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Score 603; Db 2,
    22.1%; Sco. 100.0%; Pred. No. 2. 0; Mismatches
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InterPro; IPR008984; SMAD_FHA.
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PRINTS; PR00267; INTFRNREGFCT.
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Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA sequences.
                                        Matches 109; Conservative
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                           Similarity
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                                                                                                                                                                                                                                              131 REGPGTDQTEAEAPAAVPPPQGGPPG-PFLAHTHAGLQAPGPLPAPAG-----DKGDL 182
                                                                                                                                                                                                                                                                                    | :|: |: | | 10 -----PQNHQEIGSAIQSAEAVQRQLPFIABVY---NASNHMSQDMELELLNLVETMDL 160
                                                                                                                                                                                                                                                                                                                                                                                         183 LLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVET 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 KVVGHPSCTFLYGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482
Zhang Y., Zhang Q., Xu D., Hu C., Gui J.;
"Identification of antiviral-relevant genes in the cultured fish cells induced by inactivated virus.";
Chin. Sci. Bull. 48:581-588(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 QYGIYGFRQDKCKVFVSTSDPCEIQKPEPRK--LQQNYKEQLLSFDKYIRDLLDFK-ENR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 GGSPDYTIYLCFGEKLHDGKPLEKKLITVKVVPLICRELHERAQMEGASSLRNDNVSLQI
                                                                                                                                                                    -----NDKAKWKTNFRCALHSLKNFEMLEDHSKDPDDQHKIYRIIR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 GPOLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRAROR
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
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GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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Last annotation update)
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EMBL, AY177629, AAO18646.1; -.
HSSP, P15314; 1IF1.
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MIM; 607218; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TPYPEQÇ 190
                                                                                                                                                                                                                                                                                              ----PQPAALTTGEAAAPESPHQAEPYLSPS----PSACTAVQEPSPGALDVTIMYKGR 298
                                                                                                                                                                                                                                                                                                          TVLQKVVGHPSCTFL---YGPPDPAVRATDPQQVAFPSPAELPDQKQLRYTEELLRHVAP 355
                                                                                                                                                                                                                                                                                                                                                       GLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELV 415
                                                                                                                                                                                                                                                                                                                                                                                                           GLOLEVNOYGIYGFRODKCKVFVSTSDPSEIQNPEPRK--LHQNSREQLFSFDKYIRDLM 338
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                                                                                                                                                                                                                                                 194 D----HLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSPG-- 247
                                                                                                                                   99
                                                                                                                                                                                                     134 PGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQSCLA
                                                                                                              FGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFARKDLSEADARIFKAWAVARGRWPPS
                                                                                                                            74 SRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSRELCWREG
                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                               Match 18.9%; Score 515.5; DB 2; Length 421; Local Similarity 30.3%; Pred. No. 6.1e-21; les 150; Conservative 70; Mismatches 160; Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Kidney;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grossman A., Mittrucker H.W., Lantonio L., Mak T.W.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                           605B43465FD89ABE CRC64;
                                                                                                                                                                                                                                                                        151 QVETMHLNQQS--AEPQPWDC---SQQNIQTTSRSYFG----
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                                          49056 MW;
        PRINTS; PR00267; INTFRNREGFCT
ProDom; PD002355; IRF; 1.
SMART; SM0348; IRF; 1.
SEQUENCE 421 AA; 49056 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 HKVYALSRELC------PARGPGTDQTEAEA------PAAVP 148
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A., Pahet J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schort R.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
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Poly-Glu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S., 99:16899-16903(2002).
-i. SUBCELLULAR LOCATION: Nuclear.
-i. SIMILARITY: Belongs to the IRF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.9%; Score 487.5; DB 1;
28.9%; Pred. No. 2.5e-19;
iive 59; Mismatches 173;
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PRINTS; PR00267; INTFRNREGFCT.
ProDom; PD002355; IRF; 1.
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Matches 154; Conservative
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PROSITE; PS00601; IRF; 1.
DNA-binding; Nuclear prot
DNA_BIND 16 118
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Genew; HGNC:6120; IRF5.
H-InvDB; HIX0007060; -.
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                                                                       263
                                                                                                                                            264 PHQAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVGHP-SCTFLYGPPDPAVR 322
                                                                                                                                                                                                                 ATDPQ------QVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQLWARRMG 372
                                                                                                                                                                                                                                                                                        KCKVYWEVGGPPGSASPSTPACLLPRNCDTP1FDFRVFFQELVEFRARQRRGSPRYTIYL 432
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                                                                                                        188 SPLAPP-----PGPLPASI----PGPLPASI----PPA
                                                                                                                                                                GEQLLPDLLISPHMLPLTD-----LEIKFQYRGRPPRALTISNPHGCRLFYS----QLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FKAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGD-PADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 HKVYALSRELCWREGPGTDQTEAEAPAAVPPPQGGPPG------PFLAHTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 LISPHMLPLTD-----LEIKFQYRGRPPRALTISNPHGCRLFYS----QLEATQEQVEL
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 PPQGGPP---GPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQSCLADHLLTASWGADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 GQEGLPLTGACAGGPGLPAG--ELYGWAVETTPSPGPQPAALTTGEAAAPESPHQAEPYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                 435
                                                                                                                                                                                                                                                                                                                                                             433 GFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDL 480
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Hu G., Mancl M.B., Barnes B.J.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY693665; AAUL21877.1; -
SEQUENCE 514 AA, 57770 MM; D554D121D9E35893 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 28, Created)
(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.7%; Score 482.5; DB 2;
29.6%; Pred. No. 4.9e-19;
tive 60; Mismatches 201;
                                     ------PAP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interferon regulatory factor 5 variant 5.
Name=IRF5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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nes 154; Conservative
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                                   171 PPTLOPPUVLGP
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 317
                      228 --PPAGEQLLPDLLISPHMLPLTD-----LEIKFQYRGRPPRALTISNPHGCRLFYS-- 277
                                                                     367
                                                                                         FKAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGD-PADP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 FKAWAKETGKYTEG------VDEADPAKWKANIRCALNKSRDFRLIYDGPRDMPPQP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PAAVP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 YKIY----EVCSNGPAPTDSQPPEDYSFGAGEEEEEEEELQRMLPSLSLTEDVKWPPTLQ 170
                                                                                                                                            ARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRGSPR 427
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                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrENBLrel. 27, Last sequence update)
05-JUL-2004 (TrENBLrel. 27, Last annotation update)
Interferon regulatory factor 5 variant 4 (Interferon regulatory factor 5 variant 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAPESPHOAEPYLSPSPSACTAVQEPSPGALDVTIMYKGRTVLQKVVGHP-SCTFLYGPP
                                                                     -----QVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barnes B.J., Moore P.A., Pitha P.M.;
"Vithus-specific activation of a novel interferon regulatory factor,
IRF-5. results in the induction of distinct interferon alpha genes.";
J. Biol. Chem. 276:23382-23390(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MALAPERAAPRVLFGEWLLGE1SSGCYEGLQWLDEARTCFRVPWKHFARKDLS-EADARI
                                                                                                                                                                                                                                    428 YTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor activity; IEA.
transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=21316468; PubMed=11303025; DOI=10.1074/jbc.M101216200;
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BETTALES B.J., Pitha P.M.;

L Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY504947; AAR90325.1; -.

DR EMBL; AY504946; AAR90325.1; -.

GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-depende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 HKVYALSRELC--------WREGPGTDQTEAEA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 17.7%; Score 484.5; DB 2; al Similarity 28.6%; Pred. No. 3.6e-19; 151; Conservative 59; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                            488 AA
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InterPro; IPR001346; IRF.
InterPro; IPR008984; SWAD FHA.
InterPro; IPR09058; Wing_hlx_DNA_bnd.
                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                     318 DPAVRATDPO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=IRF5;
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SEQUENCE
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QERCM8
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Name=irf3;
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                                                                       440
                           FGPISLEQVRFPSPEDIPSDKQRFYTNQLLDVLDRGLILQLQGQDDLYAIRLCQCKVFW-- 362
             -----QVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEV 380
                                                                                                 363 SGPCASAHDSCPN-PIQREVKTKLFSLEHFLNELILFQKGÖTNTPPPFEIFFCFGEEWPD 421
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96102173; PubMed=8524823; Au W.W., Juang Y.-T., Pitha P.M.; Au W.W.-C., Moore P.P.A., Lowther W.W., Juang Y.-T., Pitha P.M.; "Identification of a member of the interferon regulatory factor family that binds to the interferon-stimulated response element and activates expression of interferon-induced genes."; Proc. Natl. Acad. Sci. U.S.A. 92:11657-11661(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99020108; PubMed=9803267;
MEDLINE=99020108; PubMed=9803267;
MEDLINE=99020108; PubMed=9803267;
MEDLINE=99020108; PubMed=9803267;
MEDLINE Grown of Company factor 3 (IRF3) to chromosome 19913.3-13.4 by an intragenic polymorphic marker.";
Mun. Hum. Genet. 6:231-234(1998).
-! FUNCTION: May activate transcription by complex formation with other transcriptional factors, possibly members of the STAT family. Binds specifically to the IFN-stimulated response element (ISRE) but not to the IRF-1 binding site PRD-I.
                                                                     GGPPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSA
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 102F; X-ray; A/B=170-427.
PDB; 102F; X-ray; A/B=170-427.
PDB; 10WT; X-ray; A/B=173-427.
PDB; 10WT; X-ray; A/B=173-427.
PDB; 10WT; X-ray; A/B=173-427.
Genew; HGNC:6118; IFF3.
H-InvDB; HIX0015338; -.
MIM; 603734; F:RNA polymerase II transcription factor actic. GO; GO:0003702; F:RNA polymerase II transcription factor actic. GO; GO:0003702; F:RNA polymerase II transcription factor actic. InterPro; IPR001346; PIRE.
InterPro; IPR001946; RAD_FHA.
                                                                                                                               GRPKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDL 480
                                                                                                                                              01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
02-CCT-2004 (Rel. 45, Last annotation update)
Interferon regulatory factor 3 (IRF-3).
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                                                                                                                                                                                                                                  427
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                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 AORLGHCHTYWAVSEELLPNSGHGPDGE-----VPKDKEGGVFDLGPFIVDLITFT 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 EDILDELL-GNMVLAPLP-----SLAVAPEPCPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 PLRSPSLDNPTP----FPNLGPSENPLKRLLVPGEEWEFEVTAFYRGROVFOOTISCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64; Mismatches 191; Indels 108; Gaps
                                                                                             SMART; SW00348; IRF; 1.
PROSITE; PS00601; IRF; 1.
3D-structure; Activator; DNA-binding; Nuclear protein; Polymorphism;
Transcription regulation.
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Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                              Tryptophan pentad repeat.
R -> Q (in dbSNP:968457).
/FTId=VAR_011901.
E -> K (in dbSNP:1049486)
                                                                                                                                                                                                                                                                                                                                                                            /FTIG=VAR 011903.
427 AA; 47219 MW; P536676FA78B0110 CRC64;
                                                                                                                                                                                                                                                                                                                    /FTId=VAR 011902.
S -> T (in dbSNP:7251).
/FTId=VAR_011903.
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Interferon regulatory factor 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.8%; Score 458; DB 1; 28.0%; Pred. No. 9.3e-18;
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InterPro; IPR009058; Wing hlx DNA bnd.
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DLHISNSHPLSLTSDQYKAYLQDL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 -NSGVG----DFSQPDTSPDTNGG
                      Pfam, PF00605, IRF, 1.
PRINTS, PR00267, INTFRNREGFCT.
ProDom, PD002355; IRF, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 141; Conservative
                                                                                                                                                                                                                                             96
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                                                                                                                                                                                                                                                                                                                                                        427
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SEQUENCE FROM N.A.
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243 TPSPGPQPAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSP----
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ProDom; PD002355; IRF; 1.
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HSSP; P23906; 1IRF.
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                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 WPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGDPADPHKVYALSRELC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 WREGPGTDQTEAEAPAAVPPPQGGPPGPFLAHTHAGLQAPGPLPAPAGDKGDLLLQAVQQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----DTSLD---- DTSLD---- 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 SCLADHLLTASWGADPVPTKAPGEGOEGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 MYKGRIVLOKVVGHPSCTFLYGPPDPAVRATD----PQQVAFPSP-AELPDQKQLRYTEE 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 LLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFDFR 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 VLSCLGGGLALWRAQQWLWAQRLGHCHVYWAMGEELIPDSGHKPDGEVPKDREGGVFDLG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 VFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLEPWLCRVHLEGTQRE 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 PFIEDLIAFIEGSRR-SPRYTLWFCMGQSWPQDEPWVKRLVWVKVVPMCLRALVDMARDG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 PAALTTGEAAAPESPHQAEPYLSPSPSACTAVQEPSPGA--------LDVTI 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 SLTL-----ALEQP----PQLSLSPSVDAPASCPNLGVRENPLKQLLANDDEWEFQVTV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 FÝRGCOVFÓGTVCSÞGGLRLVGS-----BÁEDGTLAGÓPVRLÞDÞAASLTDRGVADÝVRR 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                           10 PRVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWXHFARKDLSEADARIFKAWAVARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 PRIL--PWLISQLNQGQLEGVAWLDEGHTRFRIPWKHGLRQDAQQEDFGIFQAWAEASGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 YTP----GKDKPDLPT----WKRNFRSALNRKEALRLAEDHSKDPHDPHKIYEF----
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Uenishi H., Eguchi T., Suzuki K., Sawazaki T., Toki D., Shinkai H.,
Vkumura N., Hamashima N., Awata T.;
"PEDE (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries.";
                                                                  Nucleic Acids Res. 32:D484-D488 (2004).

EMBL, AB116563; BAD06317.1; -...

EMC. GO:0005634; C:nucleus; IEA.

GO: 00:0003700; F:transcription factor activity; IEA.

GO: 00:0003155; P:regulation of transcription, DNA-dependent; IEA.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                               16.6%; Score 453.5; DB 2; Length 419; 28.4%; Pred. No. 1.6e-17; ive 55; Mismatches 176; Indels 127;
                                                                                                                                                                                                                                                                       SMART; SM00348; IRF; 1.
PROSITE; PS00601; IRF; UNKNOWN 1.
SEQUENCE 419 AA; 46645 MW; BB731861BE002284 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                             Interpro; IPR001346; IRF.
Interpro; IPR008984; SMAD FHA.
Interpro; IPR008908; Wing_hlx_DNA_bnd.
Pfam; PF00605; IRF; 1.
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Xenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                   Matches 142; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381
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072X66
1D 072X9
AC 072X9
DT 01-JU
DT 01-JU
DE MGC53
OS Eukar
OC Eukar
OC Amphi
OC Amphi
OC Amphi
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MEDLINE=2238625; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Ponaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., Morean P.J., McKernan K.J., Malek J.A., Hulyk S.W.,

A Bosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raha S.S., Loquellano N.A., Sodergren B.J., Lu X., Gibbs R.A.,

Raha S.B., Morley R.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rozywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
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GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001346; IRF.
InterPro; IPR008984; SMAD_FHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 466;
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TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 16.4%; Score 448; DB 2; Length 46 Best Local Similarity 25.0%; Pred. No. 3.6e-17; Matches 130; Conservative 94; Mismatches 205; Indels
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 466 AA; 52677 MW; 0B3A5A22C0DCDE2A CRC64;
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SEQUENCE FROM N.A.

STRAIN=AB; TISSUE=Whole body;

XI STRAIN=AB; TISSUE=Whole body;

XI Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Straubberg R.L., Feingold E.A., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worlery K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worlery K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worlery K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Generation and initial analysis of more than 15,000 full-length human and mouse C.D.
                                                                                                                                                                                                                                                             343 LRYTEELLRHVAPGLHLELRGPOLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDT 402
                                                                                                                                                                                                                                                                                                                                                           403 PIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGRPKEKSLVLVKLBPWLCRVHL 462
                                                                                                                                                                                                                                                                                                                                                                                             363 ILHTLQQFVAELTEFIERTRKSSPQYHIWMCLGELWPDVRPWNKKFIMVQIVPVSMKLLH 422
                              -----AEVATNQGSPLQQHITDHFFQDRTLR 251
                                                                                           287 GALDVTIMYKGRTVLQKVVGHPSCTFLYGPPDPAVRATDP----QQVAFPSPAELPDQKQ 342
                                                                                                                                                       252 TEPEVTVYYRGIEVSKTLVKNP----HGFRITSRKHSSPGSYLDDVVLPSPTMIADQAV 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein zgc:63500.

ORFNames=zgc:63500;
Brachydanio rerio (Zebrafish) (Danio rerio).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC056772; AAH56772.1; -..
EMBL; BC056772; AAH56772.1; -..
EMBL; BC056772; AAH56772.1; -..
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                463 EGTQREGVSSLDSSDLDLCLSSANSLYDDIECFLMELEQ 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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InterPro; IPR008984; SWAD_FHA.
InterPro; IPR009058; Wing_hlx_DNA_bnd.
                       TPAYSTAPVHMGAHAEALP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR009058; Wing_hlx_
Pfam; PF00605; IRF; 1.
PRINTS; PR00267; INTFRNEGFCT
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STRAIN=AB; TISSUE=Whole body;
Strausberg R.;
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                              207
                                                                                                                                                                                                                                                                                        307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 PVSLEQVRFPPTEHIANDKQRVFTSRLLDVMDRGLILEVSGHDIYAVRLCQCKVYW---S 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 WPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLRDNSGD-PADPHKVYALSREL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 CWREGPGTDQTEAEAPAAVP-----PPQGGPPGPFLAHTHAGLQAPGPLPAPAG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 DKGDLLLQAVQQSCLADHLLTASWGADPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----PPPALPPPAATVLPAAAAPPANVWPKKEPEDVE--MOPPP-----MEIQTPTAL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---PQQVAFPSPAELPDQKQLRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGG 382
                                                                                                                                                                                                                                                              69
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                                                                                                                                                                                                                                                           11 RVLFGEWLLGEISSGCYEGLQWLDEARTCFRVPWKHFAR-KDLSEADARIFKAWAVARGR
                                                                                                                                                                                                                                                                                                               7 RVRLKPWLVSQVDNATFPGLVWLDRDAKRFQIPWKHATRHTPQQEEENTIFKAWAVETGK
                                                                                                                                                                                                                                                                                                                                                                                                 -----LAAVW-----TPPGSVSPLQP--SSCAPPPALP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 WAVETTPSPG-POPAALTTGEAAAP-----ESPHQAEPYLSPSPSACTAVQEPSPGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----VTIMYKGRTVLQKV-VGHP-SCTFLYGPPDPAVRATD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 PPGSASPSTPACLLPRNCDTPIFDFRVFFQELVEFRARQRRGSPRYTIYLGFGQDLSAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443 PKEKSLVLVKLEPWLCRVHLEGTQREGVSSLDSSDLDLCLSSANSLYDDIECFLMEL
                                                                                                                                                                                                          129;
                                                                                                                                                      Length 492;
                                                                                                                                                                                                          Indels
                                                                         Hypothetical protein.
SEQUENCE 492 AA; 54876 MW; 98EF8FD3FE1F589B CRC64;
                                                                                                                                                   Query Match 16.3%; Score 445.5; DB 2;
Best Local Similarity 27.4%; Pred. No. 5.3e-17;
Matches 147; Conservative 74; Mismatches 187;
                     SMART; SM00348; IRF; 1.
PROSITE; PS00601; IRF; 1.
ProDom; PD002355; IRF; 1.
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6, 2005, 16:53:59 completed: May : 183 secs Search con Job time